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Perfect score:

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Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

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Sequence 26233, Application US/10536560

Sequence 26233, Application US/10536560

Sequence 26233, Application US/10536560

GENERAL INFORMATION:

APPLICAMT: ROSETTA GENOMICS LTD

TITLE OF INVENTION: GENES AND USES THEREOF

FILLE REFREENCE: 06087.0300 PCUSA3

CURRENT APPLICATION NUMBER: US/10/536,560

CURRENT PILING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 424571

SEQ ID NO 26233

LENGTH: 32
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                                       US-11-130-645A-445004
US-11-130-645A-446298
US-11-130-645A-169416
US-11-130-645A-348741
US-11-130-645A-348741
US-11-130-645A-498699
US-11-130-645A-498699
US-11-130-645A-26518
US-11-130-645A-26518
US-11-130-645A-26519
US-11-130-645A-26519
US-11-130-645A-515014
US-11-130-645A-515014
US-11-130-645A-51319
US-11-130-645A-515014
US-11-130-645A-51319
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US-11-130-645A-728884
US-11-635-706-14106
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Pred. No. 1.8e+02;
0; Mismatches 0;
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APPLICANT: ROSETTA GENOMICS LTD
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100.0%; Pre
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, ORGANISM: Homo Sapiens
US-10-536-560-26233
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Best Local Similarity
Matches 32; Conserv
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US-10-536-560-38260/c
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Sequence 390712,
Sequence 399537,
Sequence 328462,
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Sequence 175427,
Sequence 325266,
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                                                                                                                                              June 19, 2007, 13:51:18; Search time 4501 Seconds (without alignments). 578.093 Million cell updates/sec
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                   GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd.
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US-10-536-560-38260
US-10-536-560-37526
US-10-536-560-388542
US-10-536-560-388542
US-10-536-560-390712
US-11-43-428A-328462
US-11-130-645A-206881
US-11-130-645A-67631
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Maximum Match 100%
Listing first 45 summaries
                                                                                                          nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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252
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seq length: 120
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Gaps

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Result No.

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; ORGANISM: Homo Sapiens
US-10-536-560-388542
  134 CGCCCTGAGG
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LENGTH: 32
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REPERENCE: 06697.0300. PCU313
CURRENT APPLICATION NUMBER: US/10/536,560
CURRENT FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 424571
SOFTWARE: Patentin version 3.3
SEQ ID NO 175427
LENGTH: 32
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    DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
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100.0%; Pred. No. 1.8e+02;
tive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 32; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.8e+02;
ive 0; Mismatches 0;
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APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABE;
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 06087.0300.PCUS13
CURRENT APPLICATION NUMBER: US/10/536,560
CURRENT APPLICATION NUMBER: 2005-05-26
NUMBER OF SEQ ID NOS: 424871
SOFTWARE: PatentIn version 3.3
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TITLE OF INVENTION: BIOINFORMATICALLY DETECTAIN TITLE OF INVENTION: GENES AND USES THEREOF FILE REFERENCE: 60690,0300, pcrus.
CURRENT APPLICATION NUMBER: US/10/536,560
CURRENT PILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 424571
SOFTWARE: PATENTIN VERSION 3.3
SOFTWARE: PATENTIN VERSION 3.3
LENGTH: 32
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Publication No. US20060257851A1
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Best Local Similarity 100.0
Matches 32; Conservative
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Best Local Similarity 100.
Matches 32; Conservative
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-536-560-175427
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; ORGANISM: Homo Sapiens
US-10-536-560-38260
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LENGTH: 32
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10-536-560-399537/c

Sequence 399537, Application US/10536560

Sequence 399537, Application US/20518580

Publication No. US2060257851A1

APPLICANT: ROSETTA GENOMICS LTD

TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY

TITLE OF INVENTION: BENES AND USES THEREOF

FILE REFERENCE: 06087.0300: PCUS13

CURRENT APPLICATION NUMBER: US/10/536,560

CURRENT FILING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 424571
                                                                                                                                                                                                                                APPLICANT: ROSETTA GENOMICS LID
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 06087.0300. PCUS13
FILE REFERENCE: 06087.0300. PCUS13
CURRENT APPLICATION NUMBER: US/10/536,560
CURRENT FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 424571
SGOTWARE: Patentin version 3.3
SEQ ID NO 388542
LENGTH: 32
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Publication No. US20060257851A1
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENERS AND USES THEREOF
FILE REFERENCE: 666087.0300.PCUS13
CURRENT APPLICATION NUMBER: US/10/536,560
CURRENT APPLICATION NOSE: 2424571
SOFTWARE: Patentin version 3.3
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100.0%; Pred. No. 1.8e+02;
tive 0; Mismatches 0;
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32 cecerteaeerrreaeeccaeacaecreecae 1
                                                                                                                                          Sequence 388542, Application US/10536560 Publication No. US20060257851A1 GENERAL INFORMATION:
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Best Local Similarity 100.0
Marches 32, Conservative
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CORGANISM: Homo Sapiens
US-10-536-560-390712
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PRIOR APPLICATION NUMBER: US 60/665,094
PRIOR FILING DATE: 2005-03-25
PRIOR FILING DATE: 2005-03-17
PRIOR PAPLICATION NUMBER: US 60/662,742
PRIOR PAPLICATION NUMBER: US 60/593,329
PRIOR FILING DATE: 2005-03-10
PRIOR FILING DATE: 2004-12-08
PRIOR PLING DATE: 2004-12-08
PRIOR PLING DATE: 2004-11-05
PRIOR PLING DATE: 2004-11-05
PRIOR PLING DATE: 2004-11-05
PRIOR PLING DATE: 2004-11-05
PRIOR PLING DATE: 2004-11-06
PRIOR PLING DATE: 2004-11-06
PRIOR PLING DATE: 2004-11-04
PRIOR PLING DATE: 2004-11-04
PRIOR PLING DATE: 2004-11-04
NUMBER OF SEQ ID NOS: 760616
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PRIOR APPLICATION NUMBER: US 60/662,742
PRIOR FILING DATE: 2005-03-15
PRIOR PILING DATE: 2005-03-10
PRIOR PLING DATE: 2005-01-06
PRIOR PLING DATE: 2005-01-06
PRIOR PELING DATE: 2004-12-08
PRIOR PELING DATE: 2004-12-08
PRIOR PELING DATE: 2004-11-15
PRIOR PLING DATE: 2004-11-15
PRIOR PLING DATE: 2004-11-15
PRIOR PLING DATE: 2004-10-04
Remaining Prior Application data removed - See File Wrapper or PALM.
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TITLE OF INVENTION: Micrornas and Uses Thereof
FILE REFERENCE: 06097.0202.CPUS13
CHERENT APPLICATION NUMBER: US/11/130,645A
CURRENT FILING DATE: 2005-05-16
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; Pred. No. 9.3e+
11; Mismatches
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PRIOR PELING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: US 10/709,572
PRIOR PLING DATE: 2004-05-14
PRIOR FILING DATE: 2005-03-30
PRIOR FILING DATE: 2005-03-30
PRIOR APPLICATION NUMBER: US 60/665,094
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Best Local Similarity 47.1%
Matches 24; Conservative
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APPLICANT: Amir, Avniel
APPLICANT: Yael, Karov
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; ORGANISM: Homo sapiens
US-11-130-645A-206881
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SEQ ID NO 206881
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APPLICANT: Bernstein, Jeanne
TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
FILE REFERENCE: 02/23929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGATGGGAGGAAGGGTGTGGGACTTTGGAGACTGGGTCATTAAGGGCACTGCGGGTTCC 88
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                                                                                                                                                                                             Length 29;
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Publication No. US20070050146A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Itzhak
APPLICANT: Amir, Avniel
APPLICANT: Yael, Karov
TITLE OF INVENTION: Micrornas and Uses Thereof
FILE REPERENCE: G6087.202.CPUS13
CURRENT APPLICATION NUMBER: US/11/130,645A
CURRENT FILING DATE: 2005-05-16
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                                                                                                                                                                                          Ouery Match 11.5%; Score 29; DB Best Local Similarity 100.0%; Pred. No. 1.1 Matches 29; Conservative 0; Mismatches
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PRIOR APPLICATION NUMBER: PTT/USOS/16986
PRIOR FILING DATE: 2005-16
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APPLICATION NUMBER: US 10/709,577
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 399537
LENGTH: 29
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SOFTWARE: PatentIn version 3.1
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Zhu, Wei-Yong
                                                                                                                                                                                                                                                                                                         72 GGATGCAGAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Homo sapiens
US-11-443-428A-328462
                                                                                                           ; ORGANISM: Homo Sapiens
US-10-536-560-399537
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Best Local Similarity
Matches 47; Conserv
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145 TTGAGGCCAGACAGCTCGCAGTCGGGCAGAGGCGGGGGGAGAGACGAGGCGGCTCTGGC 204
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PRIOR PLING DATE: 2004-05-14
PRIOR PLING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: US 10/709,572
PRIOR APPLICATION NUMBER: US 60/666,340
PRIOR FILING DATE: 2005-03-30
PRIOR FILING DATE: 2005-03-15
PRIOR PILING DATE: 2005-03-17
PRIOR PILING DATE: 2005-03-17
PRIOR PILING DATE: 2005-03-17
PRIOR PILING DATE: 2005-03-17
PRIOR PILING DATE: 2006-03-17
PRIOR PILING DATE: 2006-03-17
PRIOR PILING DATE: 2006-01-16
PRIOR PLING DATE: 2006-12-08
PRIOR PLING DATE: 2004-11-15
PRIOR PLING DATE: 2004-11-15
PRIOR PLING DATE: 2004-11-15
PRIOR PILING DATE: 2004-11-15
PRIOR PILING DATE: 2004-11-15
PRIOR PILING DATE: 2004-11-15
PRIOR PILING DATE: 2004-11-15
PRIOR PLING DATE: 2004-11-13
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Pred. No. 1.4e+04;
0; Mismatches 52; Indels 0
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0; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Amir, Avniel
APPLICANT: Yeal, Karonov
APPLICANT: Ranit, Aharonov
TITLE OF INVENTION: Micrornas and Uses Thereof
FILE REFERENCE: 06097.0202.02013
CURRENT APPLICATION NUMBER: US/11/130,645A
CURRENT FILING DATE: 2005-05-16
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RIOR APPLICATION NUMBER: PCT/US05/16986
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LENGTH: 63
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CURRENT FILING DATE: 2006-05-
NUMBER OF SEQ ID NOS: 1034312
SOFTWARE: Patentin version 3.1
SEQ ID NO 62563
LENGTH: 113
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Best Local Similarity 51.99
warches 56; Conservative
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Best Local Similarity 71.1
Matches 32; Conservative
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US-11-130-645A-109784
                                                                                                                         TYPE: DNA
CORGANISM: Homo sapiens
US-11-443-428A-626563
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US-11-130-645A-109784/c
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TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
FILE REFERENCE: 02/23929
CURRENT APPLICATION NUMBER: US/11/443,428A
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Pred. No. 1.1e+04;
0; Mismatches 38; Indels 0;
                                                                                                      ;; Score 25.4; DB 19; Length 64;
;; Pred. No. 9.3e+03;
11; Mismatches 16; Indels
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Publication No. US20070083334A1
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SOFTWARE: Patentin version 3.1
1.DEVICE: 1.00 567727
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Best Local Similarity 47.1%;
Matches 24; Conservative 1
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Freilich, Shiri
Beck, Nili
Zhu, Wei-Yong
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Wasserman, Ald
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Mintz, Liat
APPLICANT: Xie, Hanging
         ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-130-645A-676631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-443-428A-567727
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Best Local Similarity
Matches 48; Conserv
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Best Local Similarity 49.1'
Matches 26; Conservative
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; ORGANISM: Homo sapiens
US-11-130-645A-446298
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Job time :
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PRIOR PILLING DATE: 2004-05-14
PRIOR PILLING DATE: 2005-03-30
PRIOR PILLING DATE: 2005-03-25
PRIOR PELICATION NUMBER: US 60/665,094
PRIOR PILLING DATE: 2005-03-17
PRIOR PILLING DATE: 2005-03-17
PRIOR PILLING DATE: 2005-03-17
PRIOR PILLING DATE: 2005-03-17
PRIOR PILLING DATE: 2006-01-06
PRIOR PILLING DATE: 2004-10-06
PRIOR PILLING DATE: 2004-11-06
PRIOR PILLING DATE: 2004-11-06
PRIOR PILLING DATE: 2004-11-06
PRIOR PILLING DATE: 2004-11-04
PRIOR PILLING DATE: 2004-11-04
PRIOR PILLING DATE: 2004-11-04
PRIOR PILLING DATE: 2004-11-03
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TITLE OF INVENTION: Micrornas and Uses Thereof
FILE REFERENCE: 06087.0202.CPUS13
CURRENT APPLICATION NUMBER: US/11/130,645A
CURRENT FILING DATE: 2005-05-16
PRIOR APPLICATION NUMBER: PCT/US05/16986
PRIOR APPLICATION NUMBER: US 10/709,577
PRIOR PILING DATE: 2004-05-14
PRIOR PILING DATE: 2004-05-14
PRIOR PILING DATE: 2004-05-14
PRIOR PILING DATE: 2004-05-14
PRIOR PILING DATE: 2005-03-30
PRIOR APPLICATION NUMBER: US 60/666,340
PRIOR APPLICATION NUMBER: US 60/665,094
                                                                                                                APPLICANT: Amir, Avniel
APPLICANT: Yael, Karov
APPLICANT: Ranit, Aharonov
ITILE OF INVENTION: Micrornas and Uses Thereof
FILE REPERENCE: 06087.0202.CPUS13
CURRENT APPLICATION NUMBER: US/11/130,645A
CURRENT FILING DATE: 2005-05-16
Sequence 445004, Application US/11130645A Publication No. US20070050146A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/USOS/16986
PRIOR FILING DATE: 2005-05-14
PRIOR APPLICATION NUMBER: US 10/709,577
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APPLICANT: Bentwich, Itzhak
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Yael, Karov
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US-11-130-645A-446298
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US-11-130-645A-445004
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LENGTH: 63
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APPLICANT:
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125 TTCGCGTGTCGCCCTGAGGTTTGAGGCCAGACAGCTCGCAGTCGGGCAGGGAG 177
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PRIOR APPLICATION NUMBER: US 60/593,329
PRIOR APPLICATION NUMBER: US 60/593,081
PRIOR FILING DATE: 2006-01-06
PRIOR FILING DATE: 2004-11-08
PRIOR FILING DATE: 2004-11-15
PRIOR PILING DATE: 2004-11-15
PRIOR PILING DATE: 2004-10-04
PRIOR FILING DATE: 2004-10-04
Remaining Prior Application data removed - See File Wrapper or INUMBER: PARENT FOR SEQ ID NOS: 760616
SOPTWARE: PARENTIN Version 3.3
SEQ ID NO 446298
LENGTH: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.6%; Score 24.2; DB 19; 49.1%; Pred. No. 1.9e+04;
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9.3 100 2 AX996400 AX996400 9.3 100 2 CQ874706 CQ874706 9.2 59 2 E37929 E37929 R 9.2 81 10 AY390010 AY390010	2 (CO149122 2 (CO32396 2 (CO307710 2 (CO344556 5 AFO94482	9.1 54 6 AY177451 AY177451 9.1 65 2 BD461670 BD461670 9.1 65 2 CQ531157 CQ531157 9.1 81 10 AF040860 AF040860 9.1 120 7 RV012536 HV012636	9.0 60 2 BD477333 9.0 60 2 CQ546820 9.0 110 5 HSREIINT11 9.0 66 2 CQ630945	9.0 66 2 AR472008 8.9 60 6 MUSIGXYZ	8.9 119 2 BD044455 BD043455 BD	8.8 51 2 CQ007958 8.8 51 2 CQ007958 8.8 67 2 AX899414	ALIGNMENTS	S69137 SH Homo sapiens T-cell receptor alpha-chain (TcR V alpha) mRNA,	S69137 S69137.1 GI:545967		Eukar Mamma Catar		cells: 1-cell receptor v alpha gene usage Immunology 81 (1), 15-20 (1994) 7510663 GenBank staff at the National Library of M entry (NCBI gibbsq 144559) from the origin		/db_xref="axon:9606" /tissue_type="peripheral blood" <1>98	/gene="TCR V alpha" </th <th>with sequence im paper" /codon start=1 /product="T-cell receptor alpha-chain" /protein id=AAB30241.2" /h vref="G1:1346554"</th> <th>/translation="DSATYFCAASTTNAGKSTFGSGTTLTVKPNIQ"</th>	with sequence im paper" /codon start=1 /product="T-cell receptor alpha-chain" /protein id=AAB30241.2" /h vref="G1:1346554"	/translation="DSATYFCAASTTNAGKSTFGSGTTLTVKPNIQ"
	0 0 24 0 0 25 0 26 0 27 0 27	0 0 3 3 5 8 8 9 8 9 8 9 9 9 9 9 9 9 9 9 9 9 9 9	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		4 4 4.	ር 4 4 4 4 6 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6		RESULT 1 S69137/C LOCUS DEFINITION	ACCESSION	KEYWORDS SOURCE ORGANISM		KEFEKENCE AUTHORS TITLE	JOURNAL PUBMED REMARK	FEATURES SOUICE	gene	CDS		ORIGIN
6.2.1 Biocceleration Ltd.	time 2229 Seconds out aliquments) 408 Million cell undates/sec	tcctttcgccacctcc 252	α	8: 4052000								cted by chance to have a of the result being printed, score distribution.	Description	SS9137 Homo sapien S62198 Homo sapien AP150733 Homo sapi	Ses	Se Ho	AR606935 Sequence AR701924 Sequence AX899202 Sequence BD03473 Sequence	AX184498 Sequence AX989552 Sequence
GenCore version 6.2. Copyright (c) 1993 - 2007 Bioc	OM nucleic - nucleic search, using sw model Run on: June 19, 2007, 13:14:19 ; Search tim	Title: US-10-604-726A-8797 Perfect score: 252 Sequence: 1 gggttatctgcaactgagagt	Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0 Gapop 10.1 , Gapext 1.0	mber of hits satisfying chosen par	Minimum DB seq length: 0 Maximum DB seq length: 120	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	- a	2: gb_pat::* 3: gb_ph::* 4: gb_ph::* 5: gb_pr:* 6: gb_pr:*	J. O. O.			Pred. No. is the number of results predicted by score greater than or equal to the score of the and is derived by analysis of the total score di	SUMMARIES * Result Query No. Score Match Length DB ID	27.8 11.0 98 5 26.2 10.4 98 5 25.2 10.0 109 7	24.8 9.8 92 2 2 2 2 2 4.8 9.8 92 2 2 2 4.6 9.8 103 2	8 24.6 9.8 104 2 9 24.4 9.7 119 5 10 24.2 9.6 96 11 23.8 9.4 78 2	C 12 23.8 9.4 78 2 AR606935 C 13 23.8 9.4 78 2 AR701924 C 14 23.6 9.4 72 2 AX899202 C 15 23.6 9.4 72 2 BD044735 C 15 23.6 9.4 72 2 BD04735	17 23.6 9.4 97 2 18 23.4 9.3 100 2

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AB150733.1 GI:62171551
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                                                                                           65 GTTTTCTGGATGCAGAGTCCTCTGACTCCCTCTGCCACGGGCTGAGTTTCCGGCTCCAGG 124
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1 (bases 1 to 98)

Mohapatra, S.S., Mohapatra, S., Yang, M., Ansari, A.A., Parronchi, P., Maggi, E. and Romagnani, S.

Molecular basis of cross-reactivity among allergen-specific human cells: T-cell receptor V alpha gene usage and epitope structure
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                                                                                                                           93 GATATTTGGCTTCACAGTGAGCGTAGTCCCACTCCCAAAGGTTGATTTGCCTGCATTGGT
                                                       Gaps
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Номо sapiens T-cell receptor alpha-chain (TcR V alpha) mRNA,
partial cds.
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                    Score 27.8; DB 5; Length 98; Pred. No. 2e+03; O; Mismatches 37; Indels
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                                 2e+03;
.hes 37; Indels
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'isolate="grass-sensitive individual VI
'db_xref="taxon:9606"
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/product="T-cell receptor alpha-chain"
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/db_xref="GI:13236916"
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                  11.0%;
57.5%;
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                                                        50; Conservative
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                      Query Match
Best Local (
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AB150733 109 bp DNA linear STS 27-OCT-2005 Homo sapiens DNA, STS on chromosome 10, D10S0812i, sequence tagged

site. AB150733

ACCESSION

DEFINITION

AB150733

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Tamiya,G., Makino,S., Fujimoto,K., Oka,A., Hayashi,H., Denda,A.,
Linsen,S.E., Ikuta,T., Shinya,M., Endo,T., Tomizawa,M., Tokubo,E.,
Sato,R., Takaki,A., Nagatsuka,Y., Watanabe,H., Adamoto,R.,
Makino,Y., Nakano,S., Yamamoto,A., Yoshida,K., Okamoto,K.,
Yamaquchi,D., Ishibashi,H., Yonekura,M., Takayama,S., Nakami,Y.,
Saruwatari,T., Brand,A., van Hilten,J.A., van de Watering,L.M.,
Giphart,M.J., Bahram,S., Kulski,Y.J. and Inoko,H.
Direct Submission
L. Submitted (12-DEC-2003) Hidetoshi Inoko, Tokai University School of
Medicine, Department of Genetic Information; Bohseidai, Isehara,
Kanagawa 259-1133, Japan (E-mail:Hinoko@is.icc.u-tokai.ac.jp,
Tel:81-465-93-1121, Fax:81-463-94-8884)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Whole genome association study of rheumatoid arthritis using 27 039 microsatellites
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                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Haplorrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="pooled DNA of 100 Japanese unrelated individuals sequence tagged site D10S0812!"
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/PCR conditions="denaturation 96degC 5 min, 57degC 1 172degC 1 min, 40 cycles 96degC 45 sec, 57degC 45 sec, 72degC 1 min"
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/note="sequence tagged site D10S08121"
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Pred. No. 1.4e+04;
0; Mismatches 23;
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/organism="Homo sapiens"
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/chromosome="10"
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/rpt_unit_seq="cagg"
complement(89. .109)
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Best Local Similarity 62.9%;
Matches 39; Conservative
Homo sapiens (human)
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Homo sapiens

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS TITLE

JOURNAL

LOCUS DEFINITION

RESULT 4 AX900201

source

ORIGIN

FEATURES

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PAT 11-0CT-2005
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Genes differentially expressed in human prostate cancer and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Haplorrhini,
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                                        156 CAGCTCGCAGTCGGGCAGGGAGGGCGGGGAGAGACGAGGGGGCTCTGGCCCC 207
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                                                                 13 CAGCTCGAAATCGGAGCGGAACAGCGGGGGCTTGGGAGCGGCGGCGGCGGCGCCCC 64
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                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 92)
Edwards, J.-B.D.M., Duclert, A. and Giordano, J.-Y.
Expressed sequence tags and encoded human proteins
Patent: US 6783961-A 16064 31-AUG-2004;
Genset S.A.;;
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                                                                                                                                                                              linear
Indels
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17;
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Pred. No. 1.8e+04;
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Millennium Predictive Medicine, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA
                                                                                                                                                                            AR735995 92 bp DNA
Sequence 16064 from patent US 6783961.
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0; Mismatches
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Seguence 3158 from Patent WO0160860.
CQ471292
Mismatches
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/organism="Homo sapiens"
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Homo sapiens
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35;
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AR735995
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1 (bases 1 to 92)

2 (bases 1 to 92)

3 (bases 2 to 92)

4 (bases 3 to 92)

5 (bases 4 to 92)

6 (bases 5 to 92)

7 (bases 6 to 92)

8 (bases 6 to 92)

8 (bases 7 to 92)

9 (bases 7 to 92)

8 (bases 7 to 92)
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Mammalia, Butheria, Buarchontoglires, Primates, Haplorrhini,
Catarrhini, Hominidae, Homo.
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JEAN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 CAGCTCGAAATCGGAGCGGAACAGCGGGGCTGGGAGCGGCGGCGGCGCCCC
                                                                                                                                                                                                                                                                          Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y. Expressed sequence tags and encoded human proteins Patent: EP 1033401-A 16064 06-SEP-2000; Genset (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 24.8; DB 2; Length 92;
Pred. No. 1.8e+04;
0; Mismatches 17; Indels
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                                                       AX900201 92 bp DNA Sequence 16064 from Patent BP1033401. AX900201. GI:40055115
                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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26-FEB-1999 US 60/1224
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JP 2001269182-A/11980
02-OCT-2001
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JP 2001269182-A/11980.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity 67.3%;
Matches 35; Conservative
                                                                                                                                                         Homo sapiens (human)
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61

Query Match Best Local Similarity

ORIGIN

G06F15/40 Key

source

FEATURES

C12N5/ PC C1

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Method, array and kit for detecting activated transcription factors
by hybridization array
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                                                /codon_start=1
/product="T_cell_receptor_beta_chain"
/protuct="T_eAV28660.1"
/db_xref="0f1:54111803"
/translation="NVNALLLGDSALYLCASSSGTPYGYTFGSGTRLTVVEDL"
                                                                                                                                                                                                                                                            37 CCCCAAGTIGGAAGGGCGCTTTGCTTTTTTTTGGATGCAGGCTCCTCTGACTCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unclassified.
1 (bases 1 to 96)
Han,K., Kim,D. and Kim,H.-J.
Vector-based method for visualizing secondary structure of RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 GGCGTCCCCAAGTTGGAAGGCCCTTTGCTTCTGTTTTCTGGATGCAGAGTCCTCTGACT
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     /tissue_type="herpetic skin lesion"
<1. .>119
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Pred. No. 2.5e+04;
0; Mismatches 41;
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INHA University Foundation; Inchon-si;
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AR477180
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Sequence 1 from patent US 6651010.
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/organism="unknown"
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Best Local Similarity 54.4%;
Matches 49; Conservative
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1 (bases 1 to 78)
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AR477180/c
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                                                                                          PAT 30-JAN-2004
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1 (bases 1 to 119)

Barcy,S., Huang,M.L., Corey,L. and Koelle,D.M.
Clongitudinal Analysis of Herpes Simplex Virus-Specific CD4+ Cell Clonotypes in Infected Tissues and Blood
J. Infect. Dis. 191 (12), 2012-2021 (2005)
                                                                                                                                                                                                                                                                                                     Schlegel, R., Endege, W.O. and Monahan, J.E.
Genes differentially expressed in human prostate cancer and their
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Submitted (14-SEP-2004) Laboratory Medicine, University of
Washington, 1959 N.B. Pacific Street, Rosen Bldg, Room 154,
Seattle, WA 99109, USA
Location/Qualifiers
                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleos
Mammalia, Eutheria, Euarchontoglires, Primates, Haplorrhini,
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/cell_type="Herpes simplex virus specific CD4+ T
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57.0%; Pred. No. 2.1e+04;
tive 0; Mismatches 34; Indels (
                                                                                              linear
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Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
                                                                                            CQ480460 10327 from Patent WO0160860.

    104
    /organism="Homo sapiens"
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/db_xref="taxon:9606"

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/mol_type="mRNA"
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 62 CTCTTCCTTCGCTAACGCC 80
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AY751306.1 GI:54111802
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AY751306
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PAT 18-DEC-2003

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Gaps

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Gaps

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PAT 14-MAY-2004

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109 AGTITICCGGCTCCCAGGITICGCGTGTCGCCTGAGGTTTGAGGCCAGACAGCTCGCAGTCG 168
                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Haplorrhini,
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Haplorrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y. Expressed sequence tags and encoded human proteins Patent: EP 1033401-A 15065 06-SEP-2000; Genset (FR)
                                                                                   9.4%; Score 23.8; DB 2; Length 78; 59.7%; Pred. No. 3.7e+04; tive 0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.4%; Score 23.6; DB 2; Length 72; 69.6%; Pred. No. 4.3e+04; tive 0; Mismatches 14; Indel8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Catarrhini; Hominidae; Homo.

1 (bases 1 to 72)

Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
Sequence tag and encoded human protein
Patent: JP 2001269182-A 10981 02-OCT-2001;
GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence tag and encoded human protein.
BD034735
BD034735.1 GI:22576477
                                                                                                                                                                                                                                                                                                                                           72 bp DNP
Sequence 15065 from Patent EP1033401.
AX899202

    .72
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon;9606"

    78
/organism="unknown"
/mol_type="genomic DNA"

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JP 2001269182-A/10981
02-OCT-2001
24-FEB-2000 JP 2000118773
26-FEB-1999 US 60/122487
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Homo sapiens (human)
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Matches 40; Conserva
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AX899202/c
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                                                                                                                                                                                                                                            78 AGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAGGTCAGAGGTCAGAGAGCTCAGAGCTTCAG 19
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Method for screening for drug candidates for modulating
hethor factor activity
transcription factor activity
Patent: US 6821737-A 145 23-NOV-2004;
Panomics, Inc.; Redwood City, CA
Location/Qualifiers
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 Patent: US 6696256-A 145 24-FEB-2004;
Pandmics, Inc.; Redwood City, CA
Location/Qualifiers
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Patent: US 6924113-A 145 02-AUG-2005;
Panomics, Inc.; Redwood City, CA
Location/Qualifiers
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/mol_type="genomic DNA"
                                                                 /organism="unknown"
/mol_type="genomic DNA"
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                                                                                                                                     Query Match
Best Local Similarity 59.7
Matches 40; Conservative
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1 (bases 1 to 78)
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Unclassified.
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Matches 40; Conserva
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AR606935/c
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AR701924/c
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Gaps

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PAT 27-AUG-2002

linear

72 bp

60/122487

PAT 18-DEC-2003

linear

DNA

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PI JEAN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES PI JORDAN C 12.0115/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC C12N5/10, PC C12N5/10, PC C12N5/10, C12N5/10, C12N5/10, C12N5/10, C12N5/10, C12N5/10, PC C12N5/40
                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                  Query Match 9.4%; Score 23.6; DB 2; Length 72; Best Local Similarity 69.6%; Pred. No. 4.3e+04; Matches 32; Conservative 0; Mismatches 14; Indels
                                                                                                                                                   Location/Qualifiers.
                                                                                                                                                                                                1. .72
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                        Key
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BOUICE
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Search completed: June 19, 2007, 14:28:18 Job time : 2233 secs

8 8

23.2 9.2 101 4 ABS44245 23.2 9.2 101 6 ABS18824 23.2 9.2 118 12 ACH88031 23 9.1 65 6 ABN28044 23 9.1 87 6 ABL/5509 22.8 9.0 60 6 ABM43707 22.8 9.0 117 9 ADA73750	26 22.6 9.0 66 28 22.4 8.9 119 22.2 8.8 8 8 67 32.2 8.8 8 8 67 32.2 8.8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	22.2 8.8 13 ADR50938 Adr50938 Human 22.2 8.8 102 3 AAZ60564 Aaz60564 Aneubl 22.2 8.8 102 6 ABT11892 Abt11892 PCR pro 22.2 8.8 116 2 AAV46418 Aav46418 Ribosom 22.2 8.8 115 3 AAV16203 22.2 8.8 115 3 AAV16203 Acc16203 Human Acc16203 Human Acc125369 DNA Clc		RESULT 1 ABQ76940 standard; DNA; 115 BP. X AC ABQ76940 standard; DNA; 115 BP. XX AC ABQ76940 XX
GenCore version 6.2.1 Copyright (c) 1993 - 2007 Biocceleration Ltd. OM nucleic - nucleic search, using sw model Run on: June 19, 2007, 13:10:19; Search time 372 Seconds	<pre>(without alignments)</pre>	Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0 Searched: 5620219 seqs, 3705283702 residues Total number of hits satisfying chosen parameters: 6225436	Minimum DB seq length: 0 Maximum DB seq length: 120 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Accessed_200701:* Concessed_200701:*

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The TCR of the invention has cytostatic and appoint activity. The products of the invention has cytostatic and appoint activity. The products of the invention are useful for treatment, prevention and diagnosis of had2-associated diseases, particularly tumours and leukaemia, including use for passive or active immunisation. They can also be used to screen for therapeutic agents. This sequence enocodes the polylinker Scal-Li-(Bsgl-Scal) fragment used in the construction of the fusion constructs described in the disclosure of the invention
chains of a TCR that include the antigen-recognizing sequence (ARS) of
                                   antibody specific for aa 81-88 of hdm2 (or its complex with HLA-A2-specific antibody) and a method for identifying hdm2-specific antigens
888888888888888
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Sequence 115 BP; 19 A; 33 C; 47 G; 16 T; 0 U; 0 Other;

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106 CTGAGTTTCCGGCTCCCAGGTTCGCGTGTCGCCCTGAGGTTTGAGGCCCAGACACCTCGCAG 165
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                               Length 115;
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                                                                                                                                                                                                                                                    49; Indels
                                          DB 6;
                                                                                                                                                    ..4e+03
                                          Score 25.6; DE
Pred. No. 1.4e+
0; Mismatches
                                                     10.2%;
Query Match
Best Local Similarity 52.99
Matches 55; Conservative
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1874/c AEG19874 standard; DNA; 96 (first entry) 18-MAY-2006 Temp+ DNA AEG19874; AEG19874/

ds; DNA amplification; ligase chain reaction; fluorescence; DNA detection; diagnosis; mutagenesis; DNA sequencing

Unidentified

US2006057611-A1.

30-JUN-2005; 2005US-00173902 16-MAR-2006.

30-JUN-2004; 2004US-0584665P.

(APPL-) APPLERA CORP.

Jones R; WPI; 2006-239070/25. Kao HP, Lao KQ,

Quantitating target sequences for e.g. diagnosis, comprises exponentially amplifying a target to form exponential amplicons, and linearly amplifying exponential amplicons to form linear amplicons.

Example 2; SEQ ID NO 22; 34pp; English

The present nucleic acid sequence was used in the current invention relating to quantitating target sequences by exponentially amplifying sequences in a reaction that terminates when a selected number of exponential amplicons are produced, linearly amplifying an exponential amplicons to produce linear amplicons in coupled reactions that produces a detectable signal proportional to a linear amplicon, and measuring fluorescence signals as a function of the amplification cycle number. The invention further relates to obtaining a cycle number (Ce) and a copy number of a nucleic acid amplification reaction by exponentially and linearly amplifying a target sequence in a coupled reaction under conditions in which the exponential amplification terminates before reaching a plateau and a reporter molecule generates a detectable signal

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proportional to the number of linear stranded amplicons, measuring the detectable signal as a function of cycle number, and obtaining from it the Ce value of the amplification reaction. The detectable signal is produced by a reporter molecule, where the reporter molecule is a self-cycling reaction comprising froward and reverse amplification cycling reaction comprising forward and reverse amplification primers, hydrolyzable probe. The target sequence is amplification primers, hydrolyzable probe and thermostable polymerase having 5'-3' nuclease activity, where the forward primer is in excess of the reverse cycling reaction by a least 50:1, the probe hybridizes to a target sequence 3' relative to the forward primer, where the conditions of the reaction are effective for the forward primer, probe, and target sequence to form a substrate for the nuclease activity and for the nuclease activity to hydrolyze the probe to generate the detectable signal. The melting the temperatures (Tm) of the forward primer, reverse primer and probe with the target sequence are 5 degrees C or less. The conditions terminate the exponential phase at or before the cycle number that the exponential phase at or before the cycle number that the exponential phase is capable of producing a detectable signal. The method is useful for amplifying one or more target polymucleotide sequences of an unknown polymer accurately, senaltively and specifically with high throughput the propert or property to the property and specifically with high throughput the property are not before the cycle in the property accurately, senaltively and specifically with high throughput
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 TCTGGATGCAGAGTCCTCTGACTCCCTCTGCCACGGGCTGAGTTTCCGGCTCCAGGTTCG 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            radicity using array based assays or by single-strand conformational analysis, and in diagnosis or testing. Log-linear amplification may be used to produce templates for nucleic acid sequencing or for use in mutagenesis and gene expression analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 TCCAGCTCCCGAACCCTGTGAAGACCTCCAGCAACCTCTGTATTTTCCGTGCACGGGTTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                      $$$$$$$$$$$$$$$$$$$$$$$$$$$$$
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ds; DNA amplification; ligase chain reaction; fluorescence; DNA detection; diagnosis; mutagenesis; DNA sequencing. BP. AEG19878 standard; DNA; 96 18-MAY-2006 (first entry) US2006057611-A1. Unidentified. Temp- DNA. AEG19878; RESULT 3 AEG19878

30-JUN-2005; 2005US-00173902 30-JUN-2004; 2004US-0584665P (APPL-) APPLERA CORP. 16-MAR-2006.

Lao KQ, Jones R; WPI; 2006-239070/25. Kao HP,

Quantitating target sequences for e.g. diagnosis, comprises exponentially amplifying a target to form exponential amplicons, and linearly amplifying exponential amplicons to form linear amplicons.

Giordano J;

Duclert A,

Dumas Milne Edwards J, WPI; 2000-500381/45.

(GEST) GENSET 26-FEB-1999;

21-FEB-2000; 2000EP-00200610.

99US-0122487P

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exponential amplicons are produced, linearly amplifying an exponential amplicons are produced, linearly amplifying an exponential amplicons are produced, linearly amplifying an exponential amplicon to produce linear amplicons in coupled reactions that produces a detectable signals as a function of the amplification cycle number. The invention further relates to obtaining a cycle number (Ce) and a copy number of a muleic acid amplification reaction by exponentially and linearly amplifying a target sequence in a coupled reaction under conditions in which the exponential amplification terminates before reaching a plateau and a reporter molecule generates a detectable signal proportional to the number of linear stranded amplicons, measuring the detectable signal as a function of cycle number, and obtaining the ce value of the amplification reaction. The detectable signal is produced by a reporter molecule, where the reporter molecule is a self-cullease or flap hydrolyzable probe. The target sequence is amplification at thermal cycling reaction comprising forward and reverse amplification at thermal cycling reaction comprising forward and reverse amplification are concluses eactivity, where the forward primer is in excess of the reverse concluses eactivity, where the forward primer is in excess of the reverse concluses eactivity, where the forward primer; probe, and target sequence to form a substrate for the muclease activity and for the nuclease activity to the probe to generate the detectable signal. The method is useful to the target sequence are 5 degrees C or less. The conditions terminate the exponential phase at or before the cycle number that the exponential phase at or before the cycle number that the exponential phase at or before the cycle number that the exponential phase at or before the cycle number that the exponential phase at or before the cycle number that the tendence or annifering a detectable signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for amplifying one or more target polynucleotide sequences of an unknown polymer accurately, sensitively and specifically with high throughput capacity using array based assays or by single-strand conformational analysis, and in diagnosis or testing. Log-linear amplification may be used to produce templates for nucleic acid sequencing or for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genesis and gene expression analysis. Note: The present sequence is shown in the patent but is a version of AEG19875 in the reverse (5'
                                                                                                                                                                                                        quantitating target sequences by exponentially amplifying a reaction that terminates when a selected number of
                                                                                                                                                   sequence was used in the current invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutagenesis and gene expression analysis.
Example 2; SEQ ID NO 23; 34pp; English.
                                                                                                                                                                                                                                                                                  sequences in a
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TCTGGATGCAGAGTCCTCTGACTCCCTCTGCCACGGCTGAGTTTCCGGCTCCAGGTTCG 128 rccascrcccsaacccrsasasacccrcascaaccrcrsarrrrccsacsacsses Score 25.2; DB 15; Length 96; Pred. No. 1.7e+03; 28; Indels Sequence 96 BP; 18 A; 40 C; 18 G; 20 T; 0 U; 0 Other; 0; Mismatches 10.0%; ilarity 60.0%; Conservative CGTGTCGCCC 138 Local Similarity 42; 69 129 67 Query Match Best Loca Matches $\overset{\circ}{\times}\overset{\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\overset$ 셤 à 8

Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss. Human secreted protein 5' EST, SEQ ID NO: 16064. AAC11989 standard; cDNA; 92 BP. (first entry) 06-OCT-2000 Homo sapiens AAC11989; RESULT 4

EP1033401-A2

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

2000US-0211314P.

2000US-0255281P

13-DEC-2000;

09-JUN-2000; 5-MAY-2000;

2000US-0207454P

20-FEB-2001; 2001WO-US005171

23-AUG-2001

17-FEB-2000;

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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dr primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' ends and can therefore bused to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnostic, forensic, gene therapy and chromosome mapping procedures.
They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                          diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                        5'ESTs and for
                                                                                                                                                                                                       nucleic acid that is a 5' expressed sequence tag (5' EST) for ining cDNAs and genomic DNAs that correspond to 5'ESTs and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 CAGCTCGCAGTCGGGCAGGGAGGCGGGGAGAGACGAGCGGCTCTGGCCCC 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGCTCGAAATCGGAGCGGAACAGCGGGGGCTGGGAGCGGCGGCGGCGCCC
                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 16064; 71pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 24.8; DB 3; Length 92; Pred. No. 2.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 92 BP; 19 A; 24 C; 44 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human prostate expression marker cDNA 3158.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABV03167 standard; cDNA; 103 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.88;
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ABV03167
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether progression of prostate cancer; (b) monitoring the progression of prostate cancer; (b) monitoring the progression of prostate cancer; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of an inhibit prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (g) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer; cytostatic; carcinogen; pharmacodyanamic marker; marker; gene; ss.
                                                                           Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 GGAGGGGGGGGAGAGAGAGGGGCTCTGGCCCCTTAATTGTACTTCGGGCTCGTATTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                 DB 5; Length 103;
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 103 BP; 9 A; 38 C; 30 G; 26 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                               Score 24.6; DB 5;
Pred. No. 2.6e+03;
0; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human prostate expression marker cDNA 12327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                           Claim 1; Page 581; 11750pp; English.
              Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monahan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCTCCTTTCGCCACCTCC 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         crcrrccrrcccraacgcc 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABV12336 standard; cDNA; 104 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0207454P.
2000US-0211314P.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.8%;
Best Local Similarity 57.0%;
Matches 45; Conservative
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                Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-662795/76
                                              WPI; 2001-662795/76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; prostate
pharmacogenomic
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16-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JUL-2000;
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                Schlegel R,
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Gaps ; 0 61

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                                                                                               The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether progression of prostate cancer: (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibit in prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodyanamic or pharmacogenomic marker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.
Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                  174 GGAGGGGGGGGAGAGAGGGGCTCTGGCCCCTTAATTGTACTTCGGGCTCGTATTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTACGCGGGGACGCCGCCGCCGCGCGCCCCCTGTAGTGGCCTTCGTTTCGGTTTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human colon cancer antigen encoding cDNA SEQ ID NO:3242.
                                                                                                                                                                                                                                                                                                                           Sequence 104 BP; 9 A; 39 C; 30 G; 26 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                DB 5;
                                                                                                                                                                                                                                                                                                                                                              Score 24.6; DB 5;
Pred. No. 2.6e+03;
0; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 5034-5035; 9803pp; English.
                                                                        Claim 1; Page 2030; 11750pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 CTCTCCTTTCGCCACCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCTTCCTTCGCTAACGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                  9.88;
                                                                                                                                                                                                                                                                                                                                                                                  57.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  colorectal carcinoma; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-235357/24.
P-PSDB; AAG76755.
                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200122920-A2
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03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                     45;
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                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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cc cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diesease associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome comparable to the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and Pcc carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027
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Seguence 105 BP; 24 A; 36 C; 32 G; 8 T; 0 U; 5 Other;

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                                                                      CTGCCACGGGCTGAGTTTCCGGCTCCAGGTTCGCGTGTCGCCCTGAGGTTTGAGGCCAGA 155
                                                                                                      24 CCGCNACGCCCGCAGGNACCGGTCCGGAANTCCCGGGTCGACCCACGCNTTTCNGCCAAA 83
                                      Gaps
                                     0
Score 24.2; DB 4; Length 105;
Pred. No. 3.4e+03;
0; Mismatches 38; Indels (
                                                                                                                                        156 CAGCTCGCAGTCGGGCAGGGAG 177
                                                                                                                                                                          84 CATGGCGGGCAGGACGGGGGG 105
                 53.7%;
                 Local Similarity 53.7
es 44; Conservative
                                                                        96
 Query Match
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RESULT 9 AAC10990/c ID AAC10990 standard; CDNA; 72

AAC10990;

Transcription factor-related array hybridisation probe - SEQ ID No 145. BP.

Probe, ss, transcription factor-protein complex, transcription factor, drug screening, drug identification, array hybridisation.

08-JUN-2001; 2001US-00877243. 08-JUN-2001; 2001US-00877403. 08-JUN-2001; 2001US-00877705. 08-JUN-2001; 2001US-008477738. 30-MAY-2002; 2002WO-US017408

Identifying transcription factor-protein complexes, by isolating transcription factor complexes from sample based on a specific type of factor, and identifying different proteins present in isolated complexes.

The invention comprises a method for identifying complexes between a transcription factor and another protein. The invention also comprises method for isolating DNA probes which bind to activated transcription

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factors. The methods of the invention are useful for identifying transcription factor-protein interactions. The methods of the invention are also useful for facilitating the screening and identification of new drugs, characterising their mechanism of action and screening for adverse side effects based on drug's impact expression. The present DNA sequence represents a probe used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 AGTITCCGGCTCCAGGTTCGCGTGTCGCCCTGAGGTTTGAGGCCAGACAGCTCGCAGTCG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 acciricación cacacidades de construción de contración de contració
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 78 BP; 15 A; 27 C; 15 G; 21 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.4%; Score 23.8; DB 8;
59.7%; Pred. No. 4.2e+03;
iive 0; Mismatches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 GGCAGGG 175
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expressed sequence tag; secreted protein; cDNA isolation; Human secreted protein 5' EST, SEQ ID NO: 15065. Duclert A, Giordano J; gene therapy; chromosome mapping; ss 21-FEB-2000; 2000EP-00200610. 99US-0122487P 06-OCT-2000 (first entry) Dumas Milne Edwards J, WPI; 2000-500381/45. Human; 5' EST; 26-FEB-1999; Homo sapiens EP1033401-A2 06-SEP-2000.

obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for

Claim 1; SEQ ID NO 15065; 71pp + Sequence Listing; English.

The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 3' untranslated region (UTR) sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forenaic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors

Sequence 72 BP; 9 A; 33 C; 20 G; 10 T; 0 U; 0 Other;

Biochip; gene expression; gut; diagnostic; detection; probe; ss

Escherichia coli

EP1260592-A1 27-NOV-2002.

E. coli K12 MG1655 biochip probe SEQ ID 1015.

(first entry)

18-SEP-2003

ACD69745;

ACD69745 standard; DNA; 100 BP

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ACD69745/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AAH68727-AAH73383) associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cervical cancer; cytostatic; pre-malignant condition; gene therapy;
                                                                      ö
                        Length 72;
                                                                                                                   128 GCGTGTCGCCCTGAGGTTTGAGGCCAGACAGCTCGCAGTCGGGCAG 173
                                                                                                                                                                 ccercececcecearcasecarcasecarcasecacaeaececea 13
                                                                    14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 97 BP; 7 A; 34 C; 30 G; 23 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 23.6; DB 4;
Pred. No. 5.1e+03;
                      Score 23.6; DB 3;
Pred. No. 4.7e+03;
0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                             Human cervical cancer marker nucleic acid 193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to novel genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Berger A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0189315P
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Conservative
                          9.4%;
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                                                                                                                                                                                                                                                                                    AAH68919 standard; cDNA; 97
                      Query Match
Best Local Similarity 69.6
Matches 32; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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ID AAH6
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Biochip containing probes complementary with open reading frames in Escherichia coli K12, useful for detecting gene expression and expression

Weber J;

Huber A,

Drescher B,

Donner H,

WPI; 2003-241155/24

patterns.

(MWGB-) MWG-BIOTECH AG

17-MAY-2001; 2001EP-00112179. 17-MAY-2001; 2001EP-00112179

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                                                                         containing many identical probes. The probes are nucleotide sequences of 10-80 bases, are prepared ex situ from synthetic oligonucleotides and at least one includes a segment of at least 20 bases identical with, or complementary to, a segment of an open reading frame (orf) of Escherichia (oli K12. The biochip is used for specific detection of gene expression in K12 and for determining the gene expression pattern, e.g. for diagnostic determination of which E. coli strains are present in the gut, biochip provides as comprehensive as possible detection of the K12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 shorter than probes prepared by polymerase chain reaction. ACD68731 to ACD81540 represent oligonucleotide probes used with the biochip described
                                                                                                                                                                                                                                                                                                                                                           genome, with simultaneous analysis of many different genes with a single device, and comparison of gene expression between K12 and its mutants or other E. coli strains in a single experiment. Apart from qualitative and
                                                                                                                                                                                                                                                                                                                                                                                                                                                           quantitative information about gene expression, it also allows measurements of population densities for the various strains. The use of synthetic oligonucleotides for preparation of probes allows free variation in probe length and ensures high purity (and thus selectivity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reactivity and reproducibility; also synthetic probes are generally shorter than probes prepared by polymerase chain reaction. ACD68731 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 CACGGGCTGAGTTTCCGGCTCCAGGTTCGCGTGTCGCCCTGAGGTTTGAGGCCCAGAC 156
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0
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                                                      This invention describes a novel biochip comprising probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 100 BP; 21 A; 29 C; 38 G; 12 T; 0 U; 0 Other;
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5.8e+03;
21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 23.4;
Pred. No. 5.
Claim 3; Page 168; 2004pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA; 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACD76587 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACD76587;
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ACD76587
ID ACD76
XX
AC ACD76
XX
DT 18-SE
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0

Gaps

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Indels

0; Mismatches

38;

Best Loca] Matches

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Length 97;

189 GACGAGCGGCTCTGGCCCCTTAATTGTACTTCGGGCTCGTATTGTCTCTCTTTCGCCAC 248

6 eccesaderacecedesecrienagiasecrircercrircentrircrircrircerras 65

CICC 252 69

249

SGC

RESULT 11

New strains of microorganisms that produce 2-amino-4-alkylthio-butyric acid, useful for preparing L-methionine, from simple carbon source and a mercaptan or its salt, have modified methionine synthase activity.

Example 1; SEQ ID NO 9; 68pp; French.

Soucaille PNP

Gonzales B,

Chateau M,

WPI; 2004-618123/60.

14-MAY-2003; 2003FR-00005768. 18-FEB-2003; 2003FR-00001924

FR2851255-A1.

Synthetic.

20-AUG-2004

(META-) METABOLIC EXPLORER

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containing many identical probes. The probes are nucleotide sequences of 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at least one includes a segment of at least 20 bases identical with, or complementary to, a segment of an open reading-frame (orf) of Escherichia coli K12. The biochip is used for specific detection of gene expression in K12 and for determination the gene expression pattern, e.g. for diagnostic determination of which E. coli strains are present in the gut, and to determination of which E. coli strains are present in the gut, biochip provides as comprehensive as possible detection of the K12 genome, with simultaneous analysis of many different genes with a single device, and comparison of gene expression between K12 and its mutants or other E. coli strains in a single experiment. Apart from qualitative and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quantitative information about gene expression, it also allows measurements of population densities for the various strains. The use of synchetic oligonucleotides for preparation of probes allows free variation in probe length and ensures high purity (and thus selectivity, reactivity and reproducibility); alwershiptic probes are generally shorter than probes prepared by polymerase chain reaction. ACD88731 to ACD81540 represent oligonucleotide probes used with the biochip described
                                                                                                                                                                                                                                                                                                                                                                                                              Biochip containing probes complementary with open reading frames in Escherichia coli K12, useful for detecting gene expression and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACGGGCTGAGTTTCCGGCTCCAGGTTCGCGTGTCGCCCTGAGGTTTGAGGCCAGAC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel biochip comprising probe spots, each
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chadricidedececerechechicarinescendisececesesirirerescendes 99
                                                          Biochip; gene expression; gut; diagnostic; detection; probe; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 100 BP; 13 A; 35 C; 29 G; 23 T; 0 U; 0 Other;
                    coli K12 MG1655 biochip probe SEQ ID 7863
                                                                                                                                                                                                                                                                                                                                     Weber J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 1228; 2004pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide DmetER, SEQ ID 9.
                                                                                                                                                                                                                                                                                                                                     Huber A,
                                                                                                                                                                                                                                                      17-MAY-2001; 2001EP-00112179.
                                                                                                                                                                                                                17-MAY-2001; 2001EP-00112179.
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                                                                                                                                                                                                                                                                                                                                     Drescher B,
                                                                                                                                                                                                                                                                                              (MWGB-) MWG-BIOTECH AG
                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-241155/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in the invention
                                                                                                                                   EP1260592-A1
                                                                                                                                                                           27-NOV-2002.
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                                                                                                                                                                                                                                                                                                                                     Donner H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADR28210;
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cystathionine-gamma-synthase or an acylhomoserine sulfhydrylase, and is modified so that the substrate is reacted with (II) rather than with Licysteine, to result in preferential conversion of the substrate to (I) or homocysteine. The present sequence was used in an example from the
                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a novel strain (A) of a microorganism which produces a 2-amino-4-alkylthio-butyric acid (I) by metabolising a simple sugar and a thiol (II), or its salt, and has at least one gene encoding an enzyme with modified methionine synthase (MS) activity. (A) are specifically used for fermentative production of L-methionine, which is produced from a simple carbon source and alkylmeraptan, i.e. metaported from a simple carbon source and alkylmeraptan, i.e. metaported is a toxic waste product from the petrochemical industry and synthesis of L-Met occurs in a single step from O-(acetyl or succinyl). L-homoserine. The enzyme with modified MS activity is either
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 CACGGGCTGAGTTTCCGGCTCCAGGTTCGCGTGTCGCCCTGAGGTTTGAGGCCAGAC 156
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biotransformation; NADPH-dependent enzyme; nucleic acid metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
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Pred. No. 5.8e+03;
0; Mismatches 21; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid DmetER to generate evolved microorganisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 100 BP; 15 A; 36 C; 25 G; 24 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lipid metabolism; sugar metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.3%;
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14-MAY-2003; 2003FR-00005768.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 63.2
Matches 36; Conservative
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2-amino-4-alkylthio-butyric acid; methionine synthase; cystathionine-gamma-synthase; as.

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(A) with modified metabolic pathways comprising: (a) genetic modification of a microorganism to inhibit production or consumption of a metabolite when it is grown on a defined medium, thus affecting its ability to grow; (b) growing the modified organism in the defined medium so that evolution can occur, optionally with addition of a co-substrate to allow evolution; and (c) selecting as (A) cells able to grow on the medium, optionally in presence of co-substrate. The evolved microorganisms (A), or evolved proteins (I) expressed by them, are useful in biotransformation processes, especially those involving NADH-dependent enzymes, particularly synthesis of amino acids (Met, Cys, Thr, Lys or Ile) but constructed more efficient production of selected metabolism of sugars. (A) provide more efficient production of selected metabolites than parent strains. This sequence represents a nucleic acid molecule used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                    invention relates to a method for preparing evolved microorganisms
                                                                                                                                                                                                  New evolved microorganisms with altered metabolic pathways, useful for production of amino acids, are selected as mutants able to grow defined media.
                                                                                                                Gonzalez B, Meynial-Salles I, Soucaille PNP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 100 BP; 15 A; 36 C; 25 G; 24 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                         ID NO 1; 113pp; French
14-MAY-2003; 2003FR-00005769.
06-NOV-2003; 2003FR-00013054.
                                                                 (META-) METABOLIC EXPLORER.
                                                                                                                                                              WPI; 2004-653418/63
                                                                                                                                                                                                                                                                                                           Disclosure; SEQ
                                                                                                                  Chateau M,
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                                                       100 CACGGGCTGAGTTTCCGGCTCCAGGTTCGCGTGTCGCCCTGAGGTTTGAGGCCAGAC 156
                           Gaps
                           ;
0
DB 13; Length 100;
                           Indels
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 Score 23.4; DB 13;
Pred. No. 5.8e+03;
0; Mismatches 21;
  9.3%;
               Local Similarity 63.2
nes 36; Conservative
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AAZ89260 standard; DNA; 59 BP
                                                                      (first entry)
                                                                                                                                                                                                                     Homo sapiens.
                                                                     09-JUN-2000
                                        AAZ89260;
AAZ89260,
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Human; brain; nerve degeneration; nootropic; neuroprotective; anticonvulsant; antiparkinsonian; antidabetic; treatment; infarction; Parkinson's disease; Alzheimer's disease; Huntington's disease; muscular hypoplastic lateral sclerosis; diabetic neuropathy; PCR primer; Human embryonic brain protein PCR primer #5 99WO-JP004171 WO200007614-A1 02-AUG-1999; 17-FEB-2000.

Mori A, Watanabe A;

Horie M, Hirano H, Kyushiki H, Mitsumoto Y,

(SAKA) OTSUKA PHARM CO LTD

98JP-00221886 99JP-00029164

05-AUG-1998; 05-FEB-1999;

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New protein isolated from human embryonic brain useful for treating nerve degeneration diseases e.g. Parkinson's diseases and Alzheimer's disease.
                                                                                                                                                                                  (I) which has nootropic, neuroprotective, anticonvulsant, antiparkinsonian and antidiabetic activity. (I) is useful for treating nerve degeneration diseases e.g. Parkinson's disease, Alzheimer's disease, muscular hypoplastic lateral solerosis, Huntington's disease, brain infarction, diabetic neuropathy and traumatic nerve degeneration.
                                                                                                                                                                                                                                                                                               AAZ89256-Z89234 represent PCR primers used in the isolation and amplification of the human brain protein described in the method of the
                                                                                                                                                       invention describes a novel human embryonic brain derived protein
                                                                                                                Example 2; Page 62; 69pp; Japanese
                                                                                                                                                                                                                                                                                                                                                          invention
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eful e.g.

Zink O;

credicadricecreaegeaegreegaaageaegecaectraacegeegeara 1 Search completed: June 19, 2007, 13:36:55 Job time : 376 secs 22 셤

159 CTCGCACTCGGGCAGGGAGGGCGGGGAGAGAGGGGGCGCTCTGGCCCCTTA 210

Gaps

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9.2%; Score 23.2; DB 3; Length 59; 55.4%; Pred. No. 5.8e+03; ve 0; Mismatches 18; Indels

65.48;

Query Match Best Local Similarity Matches 34; Conserv

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Conservative

Sequence 59 BP; 9 A; 23 C; 14 G; 13 T; 0 U; 0 Other;

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Sequence 16064, A
Sequence 1, Appli
                                                                                                                                                                                                     June 19, 2007, 13:32:50 ; Search time 424 Seconds (without alignments) 1112.074 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isbued Patents NA:*

1: /EMC Celerra SIDS3/ptodata/2/ina/1_COMB.seq:*

2: /EMC Celerra SIDS3/ptodata/2/ina/5_COMB.seq:*

3: /EMC Celerra SIDS3/ptodata/2/ina/6A COMB.seq:*

4: /EMC Celerra SIDS3/ptodata/2/ina/6A COMB.seq:*

5: /EMC Celerra SIDS3/ptodata/2/ina/H COMB.seq:*

6: /EMC Celerra SIDS3/ptodata/2/ina/H COMB.seq:*

7: /EMC Celerra SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*

8: /EMC Celerra SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*

9: /EMC Celerra SIDS3/ptodata/2/ina/PCTUS_Seq:*

10: /EMC Celerra SIDS3/ptodata/2/ina/PGCMB.seq:*
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GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd.
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US-09-877-705A-145
US-09-813-990C-15065
US-09-513-999C-15685
US-09-513-999C-15277
US-09-513-999C-15277
US-09-662-183A-13
US-09-513-999C-20278
US-09-513-999C-20278
US-09-513-999C-20278
US-09-113-999C-20278
US-09-165-616-57
US-09-165-616-57
US-09-165-616-57
US-10-040-497-57
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US-09-513-999C-14603
US-08-458-423A-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1403666 seqs, 935554401 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                       OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 120
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No.
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21.6 8.6 116 2 US-08-458-424B-34 Sequence 34, Appl 21.6 8.6 116 3 US-08-973-124-34 Sequence 34, Appl 21.6 8.6 116 7 PCT-US96-08014-34 Sequence 34, Appl 21.6 8.6 117 7 PCT-US96-08014-34 Sequence 63, Appl 21.4 8.5 50 3 US-10-131-827-2856 Sequence 2856, Appl 21.4 8.5 50 5 US-10-131-827-2856 Sequence 2856, Appl 21.2 8.4 107 3 US-09-621-976-8314 Sequence 18431, Appl 21.2 8.4 107 3 US-09-621-976-8314 Sequence 18431, Appl 21.2 8.4 107 3 US-09-621-976-8314 Sequence 18431, Appl 21.2 8.4 120 3 US-09-621-976-8314 Sequence 3264, Appl 21.2 8.3 47 3 US-09-621-976-831 Sequence 27, Appl 21.8 3 US-09-621-976-831 Sequence 27, Appl 21.8 3 US-09-631-992-13592 Sequence 17, Appl 20.8 8.3 118 3 US-09-634-368-16 Sequence 16, Appl 20.8 8.3 118 3 US-09-634-368-10 Sequence 27, Appl 20.8 8.3 118 3 US-09-578-291 Sequence 20, Appl 20.8 8.3 114 3 US-09-578-291 Sequence 20, Appl 20.6 8.2 100 3 US-09-578-291 Sequence 20, Appl 20.6 8.2 100 3 US-08-134-364-55 Sequence 90, Appl 20.6 8.2 100 3 US-08-134-368-16 Sequence 90, Appl 20.6 8.2 100 3 US-08-134-368-16 Sequence 6, Appl 20.6 8.2 10.8 3 US-08-134-368-16 Sequence 6, Appl 20.6 8.2 10.0 3 US-08-134-52-6 Sequence 6, Appl 20.6 8.2 10.8 3 US-08-134-368-16 Sequence 6, Appl 30.6 9.7 89-529-6 Sequence 6, Appl 30.6 9.7 89-529-6	ALIGNMENTS	ULT 1 09-513-999C-16064 equence 16064, Application US/09513999C atent No. 6783961 APPLICANT: Dumla Milne Edwards, J.B. APPLICANT: Duclert, A. APPLICANT: Duclert, A. APPLICANT: Glordano, J.Y. TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. atent No. 678361 ETHER PEREBRORE: 59-US2.REG CURRENT APPLICATION NUMBER: US/09/513,999C CURRENT APPLICATION NUMBER: US 60/122,487 PRIOR FILING DATE: 1999-02-26 NUMBER OF SEQ ID NOS: 36681 SQ ID NO 16064 LENGTH: 92 TYPE: DNA ORGANISM: Homo sapiens 09-513-999C-16064	in.	.56 CAGCTCGCAGTCGGCAGGGGGGGGGGGGAGAGGGGGTCTGGCCCC 207	1T 2 9-210-305C-1 quence 1, Application US/09210305C quence 1, Application US/09210305C GENERAL INFORMATION: APPLICANT: Inha University Foundation TITLE OF INVENTION: A vector-based method for visualizing secondary structure of RNA molecules NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS: ADDRESSE: BACHMAN & IAPOINTE, P.C. STREET: Suite 1201, 900 Chapel Street CITY: New Haven
666644446141111888886666666666666666666		99C-16064 16064, Appl 76783961 1767874710Ni 17. Dunas Mi 17. Duclert 17. Giordar 17. Giordar 16064 16064 17. Homo sap 19. Giordar 19. Gior	in.	9 6	RE LEIN 6
000 00000 0 400000000000000000000000000		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Query Match Best Local S Matches 35	ન	SULT 2 -09-210 Sequenc Patent GENER
~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~		RESULT 1 US-09-513 ; Sequence; Patent ; Patent ; APPLIC ; APPLIC ; APPLIC ; APPLIC ; PATENC ; SOFTWA ;	Query M Best Lo Matches	& 43	RESULT 2 US-09-210 ; Sequence ; Patent 1 ; GENERA

STATE: Connecticut

Gaps

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TITLE OF INVENTION: METHOD FOR SCREENING FOR DRUG CANDIDATES FOR MODULATING TRANSCRIP TITLE OF INVENTION: FACTOR ACTIVITY FILE REFERENCE: 26757-704
CURRENT APPLICATION NUMBER: US/09/877,705A
CURRENT FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 162
SOFTWARES PATENTIN VERSION 3.1
SEQ ID NO 145
LENGTH: 78
                                                                                                                                                                                                                                                                                                                                                                                                                         109 AGTITICOGGCTCCAGGITICGCGTGTCGCCCTGAGGTTTGAGGCCAGACAGCTCGCAGTCG 168
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                                                                                                                                                                                                                                                                                                                                      Score 23.8; DB 3; Length 7
Pred. No. 7e+02;
0; Mismatches 27; Indels
                                                                                                                                                                                                                                              ; FEATURE:
; OTHER INFORMATION: Hybridization probe MP74
US-09-877-705A-145
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                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial sequence
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Best Local Similarity 59.7
Matches 40; Conservative
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TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED
TITLE OF INVENTION: TRANSCRIPTION FACTORS
FILE REFERENCE: 2577-702
CURRENT APPLICATION NUMBER: US/09/877,243A
CURRENT PILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 145
LENGTH: 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 9.6%; Score 24.2; DB 3; Length 96; I Similarity 43.5%; Pred. No. 5.6e+02; 30; Conservative 11; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 78;
                                      ZIP: 06510-2802
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 23.8; DB 3; Length 7
Pred. No. 7e+02;
0; Mismatches 27; Indels
                                                                                                                  OPERATING SYSTEM: WINDOWS 95/98
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,305C
FILING DATE: 11-Dec-1998
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Hybridization probe MP74
US-09-877-243A-145
                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECTLE TYPE: oligomucleotide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-210-305C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-877-705A-145/c
; Sequence 145, Application US/09877705A
; Patent No. 6821737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-877-243A-145/c
; Sequence 145, Application US/09877243A
; Patent No. 6696256
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 96 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 9.4%;
1 Similarity 59.7%;
40; Conservative
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                                                                                                         COMPUTER: IBM
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Best Local Similarity
Matches 40; Conserva
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Best Local Similarity
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APPLICANT: Li, Jason
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APPLICANT: Li, Jason
TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED
TITLE OF INVENTION: TRANSCRIPTION FACTORS
FILE REPRENCE: 26/57-701
CURRENT APPLICATION NUMBER: US/09/877,738C
CURRENT APPLICATION DATE: 2001-06-08
NUMBER OF SEL OID NOS: 162
SOFTWARE: Patentin version 3.1
SEQ ID NO 145
LENGTH: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 AGTITICCGGCTCCAGGTTCGCGTGTCGCCCTGAGGTTTGAGGCCCAGACAGCTCGCAGTCG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 AGCTTCAGGTCAGAGGTCAGAGGCTAGCTTCAGGTCAGAGGTCAGAGAGCTAGAGTTCAG 19
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TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.4%; Score 23.8; DB 3;
59.7%; Pred. No. 7e+02;
tive 0; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: Hybridization probe MP74 US-09-877-738C-145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15065, Application US/09513999C Patent No. 6783961
US-09-877-738C-145/c
Sequence 145, Application US/09877738C
Patent No. 6924113
GENERAL INFORMATION:
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62 CTGTGCCCCACAGCCACCGCCTTCTTTCCAGATCCAGGGTCTCCAGGAGCTC 10
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OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                            9.4%; Score 23.6; DB 3; Length 72; 69.6%; Pred. No. 7.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 GCGTGTCGCCCTGAGGTTTGAGGCCAGACAGCTCGCAGTCGGGCAG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 66;
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Pred. No. 1.5e+03;
0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
CURRENT APPLICATION NUMBER: US/09/513,999C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Aeomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO.15685
LENGTH: 66
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           PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1990-02-24
NUMBER OF SEQ ID NOS: 36681
SEQ ID NO 15065
LENGTH: 72
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APPLICATION NUMBER: PCT/US01/00666
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PPILING DATE: 2001-01-30
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
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APPLICATION NUMBER: PCT/US01/00667
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APPLICATION NUMBER: PCT/US01/00668
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FILING DATE: 2001-01-30
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Sequence 15685, Application US/09866108A
Patent No. 6686188
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APPLICATION NUMBER: US 60/207,456
FILING DATE: 2000-05-26
APPLICATION NUMBER: GB 24263.6
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APPLICATION NUMBER: US 60/236,359
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Best Local Similarity 64.2%;
Matches 34; Conservative
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PENN, Sharron G.
HANZEL, David K.
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Matches 32; Conservative
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ORGANISM: Homo sapiens
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US-09-866-108A-15685
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86 CTGACTCCCTCTGCCACGGCTGAGTTTCCGGCTCCAGGTTCGCGTGTCGCCC

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                                                                                                                                     GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Duclert, A.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PATER PEFERENCE: 59.032.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: PATENT.DM
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Pred. No. 2.1e+03;
0; Mismatches 41;
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64.7%; Pred. No. 2.1e+03;
tive 0; Mismatches 18
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US-09-513-999C-23785
Sequence 23785, Application US/09513999C
; Patent No. 6783961
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APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 53.4%;
Matches 47; Conservative
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SOFTWARE: Patent.pm
SEQ ID NO 15277
LENGTH: 67
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Best Local Similarity 64.7
Matches 33; Conservative
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, ORGANISM: Homo sapiens
US-09-513-999C-15277
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ORGANISM: Homo sapiens
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US-09-347-613C-13/c
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; TYPE: DNA; ORGANISM: Homo sapiens
US-09-662-183A-13
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LENGTH: 115
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APPLICANT: Blow, Nikolaj
APPLICANT: Blow, Nikolaj
APPLICANT: Hansen, Claus
TITLE OF INVENTION: No. 6734284el Neurotrophic Factors
FILE REFERENCE: 19313-001 DIV
CURRENT APPLICATION NUMBER: US/09/662,183A
CURRENT FILING DATE: 2000-09-14
                                                                                                                                                                                                                                         APPLICANT: Hansen, Claus
TITLE OF INVENTION: No. 659313381 Neurotrophic Factors
FILE REFERENCE: NeuroSearch 19313-001
CURRENT APPLICATION NUMBER: US/09/347,613C
CURRENT FILING DATE: 1999-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 22.2; DB 3;
Pred. No. 2.4e+03;
0; Mismatches 23
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PRIOR FILING DATE: 1998-07-06
PRIOR APPLICATION NUMBER: USSN 60/092,229
PRIOR FILING DATE: 1998-07-09
PRIOR PILING DATE: 1998-08-19
PRIOR APPLICATION NUMBER: DANISH 1998 01048
PRIOR APPLICATION NUMBER: USSN 60/097,774
PRIOR APPLICATION NUMBER: 1998-10-05
PRIOR PRICING DATE: 1998-10-05
PRIOR PLING DATE: 1998-10-05
PRIOR APPLICATION NUMBER: USSN 60/103,908
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PRIOR APPLICATION NUMBER: DANISH 1998 01265
PRIOR PILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 09/347, 613
PRIOR PILING DATE: 2000-07-02
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 13
LENGTH: 102
                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: DANISH 1998 00904
PRIOR FILING DATE: 1998-07-06
PRIOR PELICATION NUMBER: USSN 60/092,229
PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: DANISH 1998 01048
PRIOR FILING DATE: 1998-08-19
PRIOR FILING DATE: 1998-08-19
PRIOR FILING DATE: 1998-08-25
PRIOR APPLICATION NUMBER: DANISH 1998 01260
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APPLICATION NUMBER: USSN 60/103,908
FILING DATE: 1998-10-13
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; Sequence 13, Application US/09662183A
; Patent No. 6734284
Sequence 13, Application US/09347613C
Patent No. 6593133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 61.0%;
Matches 36; Conservative
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NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                     APPLICANT: Johansen, Teit E. APPLICANT: Blom, Nikolaj
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
US-09-347-613C-13
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169 GCCAGGGAGGGCGGGGAGAGAGAGGGCGCTCTGGCCCCTTAATTGTACTTCGGGCTCG 227
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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
Patent No. 6783961
CURRENT APPLICATION NUMBER: US/09/513,999C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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     Length 102;
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                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: RAINWEG, MITTLERER
APPLICANT: GRUMMT, FRIEDERICK
APPLICANT: VAN DER VOGELWEIDE STRASSE, WALTHER
TITLE OF INVENTION: EXPRESSION VECTOR FOR THE PERMANENT
TITLE OF INVENTION: EXPRESSION OF FOREIGN DNA
FILE REFERENCE: 352800430500
CURRENT APPLICATION NUMBER: US/09/367,927A
CURRENT FILING DATE: 1999-10-20
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Pred. No. 2.4e+03;
0; Mismatches 23;
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64.7%; Pred. No. 2.4e+03;
tive 0; Mismatches 18;
Score 22.2; DB 3;
Pred. No. 2.4e+03;
0; Mismatches 23;
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US-09-513-999C-20278/c
; Sequence 20278, Application US/09513999C
; Patent No. 6783961
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PRIOR FILING DATE: 1999-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09367927A
Patent No. 6300126
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Best Local Similarity 61.0%;
Matches 36; Conservative
               8.8%;
          Query Match
Best Local Similarity 61.0<sup>3</sup>
Matches 36; Conservative
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SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRGANISM: Homo sapiens US-09-367-927A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
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Best Local Similarity
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; ORGANISM: Homo so
US-09-513-999C-20278
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63 GGTGGGGGCGCCCGGGAGAGACACCACCTCGCAGCCCCAGAATTTGTTTTCGCTTTCG 5

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84 CTCTGACTCCCTCTGCCACGGGCTGAGTTTCCGGCTCCAGGTTCGCGTGTCGCCCTGAGG 143
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32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER TRANSLE FORM:
COMPUTER TRANSLE FORM:
COMPUTER I DISKETC, 3 1/5 inch; 1.44 MB
COMPUTER I EN Compatible
COMPUTER: DISKETCH ISS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
FILING DATE: 21-CCTOBER-1992
CLASSIFICATION WHERE: 07/714,131
FILING DATE: 10-JUNE-1991
FILING DATE: 10-JUNE-1991
FILING DATE: 10-JUNE-1991
FILING DATE: 11-JUNE-1991
FILING DATE: 11-JUNE-1990
ATTORNEY APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY AGENT INFORMATION:
WANTO DATE: 11-JUNE-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 57, Application US/08442062
Patent No. 5595877
GENERAL INFORMATION:
APPLICANT: GOLD, LARRY M.
APPLICANT: TUERK, CRAIG
TITLE OF INVENTION: ACIDS ON THE BASIS OF
                                                                                                                                                                         METHOD OF SELECTING NUCLEIC
                                                                                                                                                                                                                                                                                           E: Swanson & Bratschun, L.L.C.
8400 E. Prentice Avenue, Suite 200
                                                                                                                                                                                   ACIDS ON THE BASIS OF STRUCTURE
RESULT 14
US-07-964-624D-57/c
; Sequence 57, Application US/07964624D
; Patent No. 549698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEXOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 571
SEQUENCE CHARACTERISTICS:
                                                                                            GENERAL INFORMATION:
APPLICANT: GOLD, LARRY M.
APPLICANT: TUERK, CRAIG
TITLE OF INVENTION: METHOD
TITLE OF INVENTION: ACIDS OF INVENTION: STRUCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 TTTGAGGCCAGAC 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 86 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
US-07-964-624D-57
                                                                                                                                                                                                                                                                                                                                                                      Colorado
                                                                                                                                                                                                                                                                                                                                           Englewood
                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 80111
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US-08-442-062-57/c
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STREET: 84
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84 CTCTGACTCCCTCTGCCACGGGCTGAGTTTCCGGCTCCAGGTTCGCGTGTCGCCCTGAGG 143
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                 ALUNESSEE: Swanson & Bratschun, L.L.C. STREET: 8400 B. Prentice Avenue, Suite 200 CITY: Englewood STATE: Colorado
                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/5 inch, 1.44 MB
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: June 19, 2007, 13:59:35 Job time: 424 secs
                                                                                                                                                                                                                                                       SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,062
FILING DATE:
                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Barry J. Swanson
REGISTRATION NUMBER: 33.215
REFERENCE/DOCKET NUMBER: NEX
TELECOMMUNICATION:
TELEPHONE: (303) 793-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.7%;
Best Local Similarity 56.2%;
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 TTTGAGGCCAGAC 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 base pairs
NUMBER OF SEQUENCES: 8:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson &
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EDNESS: single
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                                                                                                                            COUNTRY:
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Sequence 9222, Ap Sequence 9222, Ap Sequence 21889, A Sequence 12025, A Sequence 20336, A

Sequence 57, Appl Sequence 57, Appl Sequence 32, Appl Sequence 34, Appl Sequence 23937, A Sequence 725, App

Sequence 2865, Ap Sequence 3692, Ap Sequence 1425, Ap Sequence 817, App

Sequence 387,

Perfect score:

Sequence:

OM nucleic -

Run on:

Scoring table:

Minimum DB Maximum DB

Database

Sequence 16455, A Sequence 15685, A Sequence 15685, A Sequence 142012, Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl

Sequence 792, App Sequence 4883, Ap

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Sequence 16611, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06687.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 16611
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Pred. No. 2e+02;
0; Mismatches 5; Indels
US-10-764-324-6323

US-09-864-761-27544

US-10-029-386-21226

US-09-908-975-792

US-09-908-975-792

US-09-908-975-16455

US-09-806-108-15685

US-10-723-361-15685

US-10-723-361-15685

US-10-723-361-15685

US-10-425-113-142012

US-10-661-984A-13

US-10-661-984A-13

US-10-806-793-13

US-10-914A-2865

US-10-310-914A-2865

US-10-310-914A-2865

US-10-310-914A-3692

US-10-310-914A-3692

US-10-310-914A-3692

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US-10-310-914A-3692

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US-10-310-914A-3692

US-10-310-914A-12025

US-10-9864-761-21889

US-10-310-914A-12035

US-10-310-914A-12035

US-10-310-914A-12035

US-10-310-914A-12035

US-10-310-914A-12035

US-10-310-914A-12035

US-10-310-914A-12035

US-10-310-914A-12035

US-10-918-063-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: KAO, H. PIN
APPLICANT: LAO, KAI QIN
APPLICANT: JONES, ROBERT
TITLE OF INVENTION: LOG-LINEAR AMPLIFICATION
FULE REPERENCE: 375461-021US
CURRENT APPLICATION NUMBER: US/11/173,902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-11-173-902-22/c
; Sequence 22, Application US/11173902
; Publication No. US20060057611A1
; GENERAL INFORMATION:
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85.7%;
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Best Local Similarity
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US-10-310-914A-16611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30;
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2: / FBMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: / FBMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
4: / FBMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: / FBMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: / FBMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
7: / FBMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: / FBMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
10: / FBMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
11: / FBMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
12: / FBMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: / FBMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: / FBMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
14: / FBMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: / FBMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
16: / FBMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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Sequence 22, Appl
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Sequence 6323, 1
Sequence 6323, 1
Sequence 6323, 1
Sequence 6323, 1
                                                                                                                                                                                                                                                                                                                  June 19, 2007, 13:37:11 ; Search time 3937 Seconds (without alignments) 786.509 Million cell updates/sec
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                                                      GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd
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US-10-357-930-3158
US-10-357-930-3158
US-10-106-698-3252
US-10-310-914A-17067
US-09-877-705A-145
US-09-877-705A-145
US-09-877-738A-145
US-09-877-403A-145
US-10-779-595-145
US-10-781-499-1
US-10-796-692-6323
US-10-40-862-6323
US-10-610-4758-6323
US-10-610-4758-6323
US-10-610-4758-6323
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                                                                                                                                                                                                                                     nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-604-726A-8797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seg length: 0
seg length: 120
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Result

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APPLICANT: Endege, Wilson
APPLICANT: Endege, Wilson
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, REEVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REPRENCE: MRI-0078CM
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 GGAGGGGGGGGAGAGAGGGGCTCTGGCCCCTTAATTGTACTTCGGGCTCGTATTGT 233
42 CTGAGTTTTCAGGCAGGCAGGCAGGCAGGCAGGCAGGTAGAGTACAGCA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 denacecedesasacecedesecedesis de la constanta de la contra del la contra della co
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Pred. No. 1.2e+03;
0; Mismatches 34;
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APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
ITILE OF INVENTION: IDENTIFICATION, ASSESSME; TITLE OF INVENTION: HOWNE RESCRIPTION OF INVENTION: HOMAN PROSTATE CANCER FILE REFERENCE: MRI-007BCN; CURRENT APPLICATION WUMBER: US/10/357,930 CURRENT FILING DATE: 2003-02-04; PRIOR FILING DATE: 2003-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR PLILING DATE: 2003-02-16
PRIOR FILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR PILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-19
PRIOR FILING DATE: 2000-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3158, Application US/10357930 Publication No. US20040259086A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 CICICITITGGCCACCICC 252
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Best Local Similarity 57.0%;
Matches 45; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Schlegel. Robert
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US-10-357-930-3158
                                                                                                                                                                    198 CT 199
                                                                                                                                                                                                                                                                   102 CT 103
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CHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
OTHER INFORMATION: Sequence listing upward to telomere on chrosomal short arm and
COTHER INFORMATION: 5'-terminus of this base sequence: 79419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 TCTGGATGCAGAGTCCTCTGACTCCCTCTGCCACGGGCTGAGTTTCCGGCTCCAGGTTCG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 iccaderecedaecergraagaeereageaaeerergrarrireegraegeaerree 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: INCAM, ALGENCEMENT APPLICANT: INCAM, ALGENCEMENT APPLICANT: INCAMINA, GENE MAPPING METHOD USING MICROSATELLITE TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE TITLE OF INVENTION: GENE MAPPING METHOD USING MARKERS FILE OF INVENTION: GENE MAPPING GENE COURTENT PLING DATE: 2003-09-26 FILE REPERSON NUMBER: US/10/57,511 PRIOR APPLICATION NUMBER: PCT/JP00/07621 PRIOR APPLICATION NUMBER: PCT/JP00/07621 PRIOR APPLICATION NUMBER: JP2000-112699 PRIOR FILING DATE: 2000-04-13 PRIOR PRILING DATE: 2000-04-13 PRIOR PRILING DATE: 2000-04-13 PRIOR APPLICATION NUMBER: JP2002-387516 PRIOR APPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 10.0%; Score 25.2; DB 16; Length 96; Similarity 60.0%; Pred. No. 7.8e+02; 42; Conservative 0; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.0%; Score 25.2; DB 9; Length 1:
62.9%; Pred. No. 7.9e+02;
tive 0; Mismatches 23; Indels
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OTHER INFORMATION: Located on chromosome 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16551, Application US/10674124A Publication No. US20040197797A1 GENERAL INFORMATION:
APPLICANT: INOKO, Hidetoshi
                                          PRIOR APPLICATION NUMBER: 60/584,665
PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.3
SEQ ID NO 22
LENGTH: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: DISD22 0010457
                               2005-06-30
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 62.99
Matches 39; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                               CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-11-173-902-22
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APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 145, Application US/09877705A
Publication No. US20030008283A1
GENERAL INFORMATION:
APPLICANT: Li, Jason
TITLE OF INVENTION:
FILE REPRENCE: 26757-704
CURRENT FILICATION UNMBRE: US/09/877,705A
CURRENT FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 162
SOFTWARE: Patentin version 3.1
SEQ ID NO 145
LENGTH: 78
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Length 105;
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Pred. No. 2.1e+03;
0; Mismatches 27; Indels
                                                 38; Indels
                                                                                                  96 CTGCCACGGGCTGAGTTTCCGGCTCCAGGTTCGCGTGTCGC
  DB 6;
Query Match 9.6%; Score 24.2; DB 6; Best Local Similarity 53.7%; Pred. No. 1.6e+03; Matches 44; Conservative 0; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 24; DB 11;
Pred. No. 1.9e+03,
7; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , OTHER INFORMATION: Hybridization probe MP74
US-09-877-705A-145
                                                                                                                                                                                                                                                                                                                                                     Sequence 17067, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
                                                                                                                                                                                               156 CAGCTCGCAGTCGGCCAGGGAG 177
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Best Local Similarity 51.8<sup>a</sup>
Matches 29; Conservative
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Best Local Similarity 59.77
Matches 40; Conservative
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Sequence 3252, Application US/10106698

Publication No. US20030109690A1

GENERAL INFORMATION:
TITLE OF INFORMATION:
TITLE OF INFORMATION:
CURRENT APPLICATION NUMBER: US/10/106,698

CURRENT APPLICATION NUMBER: D-CJ-03-27

PRIOR APPLICATION NUMBER: PCT/US00/26524

PRIOR PELING DATE: 2000-09-28

PRIOR PELING DATE: 1099-09-29

PRIOR PELING DATE: 1099-09-29

PRIOR PELING DATE: 1999-10-3

PRIOR PELING DATE: 1999-10-3

NUMBER: US 60/163,280

PRIOR PILING DATE: 1999-11-03

NUMBER: PSEQ ID NOS: 8564

SOFTWARE: Patentin Ver: 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR PLING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR PLING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR PLING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR PLING DATE: 2000-07-18
PRIOR PLING DATE: 2000-12-13
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc_feature
LOCATION: (77)...(77)
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; OTHER INFORMATION: n equals a, t, g,
US-10-106-698-3252
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
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                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-12327
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ORGANISM: Homo sapiens
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Best Local Similarity
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APPLICANT: Li, Jason
TITLE OF INVENTION: METHOD FOR IDENTIFYING A DISEASE STATE BASED ON A DETECTED MIXTUR
TITLE OF INVENTION: ACTIVATED TRANSCRIPTION FACTORS
TITLE OF INVENTION: ACTIVATED TRANSCRIPTION FACTORS
FILE REFERENCE: 26757-703
CURRENT APPLICATION NUMBER: US/09/877,403A
CURRENT FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PatentIn version 3.1
SEQ ID NO 145
LENGTH: 78
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TITLE OF INVENTION: METHOD, ARRAY AND KIT FOR DETECTING ACTIVATED TRANSCRIPTION FACTO
FILE REPERBURE: 2675-702.301
CURRENT PELLING DATE: 2004-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 AGTITICCGGCTCCCAGGTTCGCGTGTCGCCTGAGGTTTGAGGCCAGACAGCTCGCAGTCG 168
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Pred. No. 2.1e+03;
0; Mismatches 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , OTHER INFORMATION: Hybridization probe MP74
US-10-779-595-145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Hybridization probe MP74
US-09-877-403A-145
                                                                                                                                                         Sequence 145, Application US/09877403A Publication No. US20040214166A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/877,243 PRIOR FILING DATE: 2001-06-08 NUMBER OF SEQ ID NOS: 162 SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-779-595-145/c
; Sequence 145, Application US/10779595
; Publication No. US20040132090A1
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Best Local Similarity 59.7%;
Matches 40; Conservative
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169 GGCAGGG 175
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Best Local Similarity
Matches 40; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 GGCAGGG 175
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                                           18 GTCAGAG 12
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                                                                                                                                        US-09-877-403A-145/c
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TITLE OF INVENTION: METHOD FOR DETECTING TRANSCRIPTION FACTOR-PROTEIN INTERACTIONS
FILE REFERENCE: 2675-705
CURRENT APPLICATION NUMBER: US/09/947,274
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US 09/877,243
PRIOR APPLICATION NUMBER: US 09/877,243
PRIOR APPLICATION NUMBER: US 09/877,403
PRIOR FILING DATE: 2000-06-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Publication No. US20030022173A1
GENERAL INFORMATION:
APPLICANT: Li, Jason
TITLE OF INVENTION METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED
TITLE OF INVENTION: TRANSCRIPTION FACTORS
FILE REFERENCE: 26757-701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 AGTTTCCGGCTCCAGGTTCGCGTGTCGCCCTGAGGTTTGAGGCCAGACAGCTCGCAGTCG 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 23.8; DB 3; Length 78;
Pred. No. 2.1e+03;
0; Mismatches 27; Indels
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US-09-877-738A-145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Hybridization probe MP74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 145, Application US/09877738A Publication No. US20030022173A1
                                                                                                                Sequence 145, Application US/09947274
Publication No. US20030017499A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial sequence
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ORGANISM: Artificial sequence
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Best Local Similarity
Matches 40; Conserv
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  GTCAGAG 12
                                                                                                                                                                GENERAL INFORMATION
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US-09-877-738A-145/c
                                                                                               US-09-947-274-145/c
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SEQ ID NO 145
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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Marc
APPLICANT: Reteer, Marc
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
TITLE OF INVENTION: Hematological Malignancies
CURRENT APPLICATION NUMBER: US/10/040,862
CURRENT PILING DATE: 2001-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                  53 AGGTTTGGATGCAAGATGCTCTGGGAAGTGCACGCAGATATGGGGGGAGAAAAGCTGCTC 112
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Pred. No. 3e+03;
0; Mismatches 26;
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PRIOR PILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR PLING DATE: 2000-04-27
PRIOR PLING DATE: 2000-04-28
PRIOR PLING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-05-01
PRIOR PLING DATE: 2000-05-01
PRIOR PLILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR PILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223,378
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 6323
LENGTH: 120
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PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
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PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
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PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 10467
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PRIOR FILING DATE: 2000-08-04
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 60.04
Matches 39; Conservative
                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
US-09-796-692-6323
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ORGANISM: Homo sapiens
US-10-040-862-6323
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                                                                                                                                          TITLE OF INVENTION: Method for the preparation of an evolved microorganism for the critical invention: Method for the preparation of an evolved microorganism for the critical OF INVENTION: Method for the preparation of metabolic pathways

TITLE OF INVENTION: or modification of metabolic pathways

TITLE REFERENCE: D20701/345774

CURRENT APPLICATION NUMBER: U8/10/781,499

CURRENT FILING DATE: 2004-02-18

PRIOR APPLICATION NUMBER: FR 0310924

PRIOR FILING DATE: 2003-05-14

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

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Pred. No. 3e+03;
0; Mismatches 21; Indels
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; Sequence 6323, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
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APPLICATION NUMBER: 60/186,126
FILING DATE: 2000-03-01
APPLICATION NUMBER: 60/190,479
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APPLICATION UNDBER: 60/200,545
FILING DATE: 2000-04-27
APPLICATION NUMBER: 60/200,303
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APPLICATION NUMBER: 60/200,999
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APPLICATION NUMBER: 60/200,779
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Best Local Similarity 63.2%;
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Gaps
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Query Match

9.3%; Score 23.4; DB 6; Length 120;
Best Local Similarity 60.0%; Pred. No. 3e+03;
Matches 39; Conservative 0; Mismatches 26; Indels 0
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200	112
141 AGGTTTGAGGCCAGACAGCTCGCAGTCGGGCAGGGAGGGGGGGG	53 AGGTTTGGATGCAAGATGCTCTGGGAAGTGCACGCAGATATGGGGGGGAAAAAGCTGCTC 112

²⁰¹ TGGCC 205

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¹¹³ AGACC 117

Search completed: June 19, 2007, 18:07:52 Job time : 3939 secs

25.2 10.0 103 7 AM800261 25.2 10.0 103 12 EC523717 25.2 10.0 112 5 BY857392 25 9.9 100 12 DV900899	19 25 9.9 108 21 24.8 9.8 116 22 24.8 9.8 120 24.6 9.8 107 24 6 9.8 107 24 24.6 9.8 109	24.6 9.8 119 16 BZ987003 24.4 9.7 109 13 DV552589 24.4 9.7 119 13 DN773586	24.2 9.6 83 12 EC134983 24.2 9.6 104 9 CN071764 24.2 9.6 115 17 CM117487 24.2 9.6 117 18 DITI88381	33 24 9.5 100 9 CK005996 35 24 9.5 100 17 CL952595	24 9.5 101 8 CD029354 24 9.5 102 16 CC376448 24 9.5 105 9 CK451897	24 9.5 116 8 CF741809 23.8 9.4 85 12 EC429664 23.8 9.4 93 9 CK100624 23.8 9.4 101 3 BJ965328	23.8 9.4 102 3 BJ955717 23.8 9.4 102 3 BJ970068 23.8 9.4 103 3 BJ967675	ALIGNMENTS	RESULT 1	LOCUS AZ769498 100 bp DNA linear GSS 16-FEB-2001 DEFINITION IMMSFORKISF MOUSE 10kb plasmid UNGCIM library Mus musculus genomic	ACCESSION AZ769498 GI:12889695 KEYWORDS GSS	Σ	Mammala: Butheria: Burrchontoglires; Glires; Rodent Sciurognathi; Muroidea; Muridae; Murinae; Mus.	KEFEKENCE I (Dases I to luu) AUTHORS Dunn, D. Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Kose, R., Stokes, R., Tingey, A., von	JOORNAL Unpublished (2000) COMMENT Contact: Robert B. Weise University of Utah Genome Center	University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT 84112, USA	tics.utah.ed	Plate: 0570 row: K column: 16 Seq primer: CGTTGTAAAACGACGGCCAGT Class: plasmid ends Hich quality sequence stop: 100.	Location/Qualifiers 1100 /organism="Mus musc
GenCore version 6.2.1 Copyright (c) 1993 - 2007 Biocceleration Ltd.	OM nucleic - nucleic search, using sw model Run on: June 19, 2007, 13:30:48; Search time 12307 Seconds (without alignments) 1270.361 Million cell undates/sec	tecttegecaectee 252	Scoring table: IDENTITY NUC Gapext 1.0	Searched: 53585215 seqs, 31020513797 residues Total number of hits satisfying chosen parameters: 1909528	Minimum DB seq length: 0 Maximum DB seq length: 120	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries		3: gb_est4:* 4: gb_est5:* 5: gb_est6:* 6: gb_bst6:*		-	12: 95_612: 13: 95_est12:* 14: db_est10:*			Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		29 11.5 100 15 AZ769498 AZ769498 1 28.6 11.3 103 12 EC491510 EC491510 1 28 11.1 97 12 EC465112 EC465112 EC465112 2 27.6 11.0 17 12 EC465112 EC46511	4 2/2 11:0 103 1/ CG5/465/ CG5	25.8 10.2 110 9 CK014560 CK014560 25.8 10.2 110 17 CL952591 CL952591 25.8 10.2 111 12 EB652145 EB652145 25.8 10.2 113 12 EC536793 EC5336793	25.6 10.2 99 7 AV841732 AV841732 AV 25.6 10.2 103 18 DU408432 DU408432 1 25.6 10.2 117 17 CG255380 CG255380

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RESULT 3
EC465112/c
LOCUS
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KEYWORDS
SOURCE
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library Homo sapiens cDNA similar to
ENSG0000197152|ENST00000356485, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bainbridge_M.N., Warren,R.L., Hirst,M., Romanuik,T., Zeng,T., Go,A., Delany,A., Griffith,M., Hickenbotham,M., Magrini,V, Mardis,E.R., Sadar,M.D., Siddiqui,A.S., Marra,M.A. and Jones,S.J.M. Analysis of the prostate cancer cell line LNCaP transcriptome using a sequencing-by synthesis approach
                                                                                                                                                            (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.05 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative
                                                                                                                                                                                                                                                                                                                                                                                  of pwD42 (gi|4732114|gb|AF129072.1) a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adaptored vector DNA; and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia; Butheria; Buarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
                                                              /clone lib="Mouse 10kb plasmid UUGCIM library"
/notes="Vector: PWD42hv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST was generated using 454 life sciences sequence-by-synthesis
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//Lissue type="prostate"
/cell_line="LNCap"
/clone_line="LNCAp" + R1881 synthetic Androgen human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 GAGGCCAGACAGCTCGCAGTCGGCAGGGAGGCCGGGGAGAGACGAGCGCT 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 11.5%; Score 29; DB 15; Length 100; 1 Similarity 71.7%; Pred. No. 3.6e+03; 38; Conservative 0; Mismatches 15; Indels
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                                            host="E. Coli strain
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'clone="UUGC1M0570K16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             location/Qualifiers
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EC491510.1 GI:109531102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Steven Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
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Culture Collection, Bethesda, MD) were maintained in RPMI-1640 media (StemCell Technologies; Vancouver, BC) supplemented with 10% fetal bovine serum (FBS; StemCell Technologies) and incubated at 37C with 5% CO2. Cells at passage 38 were plated at a density of approximately 4X10 6 cells per T175 flask. Cells were serum-starved for 48 hours prior to treatment for 16 hours with 10 nM R1881 (PerkinElmer; Woodbridge, Canada). Cells were harvested and total RNA was extracted from the cells using TRIZOL Reagent (Invitrogen Life Technologies, Carlsbad, CA) following the manufacturer's instructions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bainbridge, M.N., Warren, R.L., Hirst, M., Romanuik, T., Zeng, T., Go, A., Delany, A., Griffith, M., Hickenbotham, M., Magrini, V., Mardis, E.R., Sadar, M.D., Siddiqui, A.S., Marra, M.A. and Jones, S.J.M. Analysis of the prostate cancer cell line LNCaP transcriptome using unpublished (2006)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EC465112.
2T010516 3708 0837 LNCAP + R1881 synthetic Androgen human prostate library Homo Sapiens cDNA similar to ENSG00000077235 ENST0000356183, mRNA sequence.
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Mammalia; Butheria; Buarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
1 (bases 1 to 97)
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EST was generated using 454 life sciences sequence-by-synthesis
'note="LNCaP human prostate cancer cells (American Type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 cccrerrecadacrecrirrirrirrirrirrirandadesendrirecriedadese
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/cell_line="LNCap"
/clone_lib="LNCAP + R1881 synthetic Androgen human
prostate_library"
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Pred. No. 4.7e+03;
0; Mismatches 39
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/db_xref="taxon:9606"
/sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 11.3%;
1 Similarity 57.1%;
52; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens (human)
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Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Finch, R.P., Piggott, J., BeltrandelRio, H., Buxton, B.C., Edwards, J., Finch, R.A., Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Fry, B.W., Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qiann, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.

Zhu, Q., Person, C. and Sands, A.T.

Minkl kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
                                                                                                                                                                                                                                        53
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(PerkinElmer; Woodbridge, Canada). Cells were harvested and total RNA was extracted from the cells using TRIZOL Reagent (Invitrogen Life Technologies, Carlsbad, CA) following the manufacturer's instructions"
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Pred. No. 8.9e+03;
0; Mismatches 19; Indels 0
                                                                                                                     Length 97;
                                                                                                                   Score 28; DB 12; Length 97
Pred. No. 6.9e+03;
0; Mismatches 35; Indels
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/clone_lib="Mus musculus 1295v/Ev"
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/clone="OST207730"
                                                                                                                                                                                                                                                                               188 AGACGAGCGCTCTGGCCCTTAA 211
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1. .103
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/strain="129Sv/Ev"
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larity 58.3%;
Conservative
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1 Similarity 67.2%;
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CG574657
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49; Conserve
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RESULT

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EE366986 110 bp mRNA linear EST 14-AUG-2006
LB02989.CR_P21 GC_BGC-29 Bos taurus cDNA clone IMAGE:8486471, mRNA
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Site_2: NotI (3' end of cDNA)" _ .
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                                                                                                                                                                                                                                                                                                                                                                                               Moore, S., Alexander, L., Brownstein, M., Guan, L., Lobo, S., Meng, Y., Tanaguchi, M., Wang, Z., Yu, J., Prange, C., Schreiber, K., Shenmen, C., Wagner, L., Bala, M., Barbazuk, S., Barber, S., Babkaiff, R., Beland, J., Chun, E., Del Rio, L., Gibson, S., Hanson, R., Tsirkpatrick, R., Liu, J., Matsuo, C., Mayo, M., Santos, R., Stott, J., Tsai, M., Wong, D., Siddiqui, A., Holt, R., Jones, S.J. and Marra, M.A. Bovine, Genome, Sequencing Program: Full-length cDNA Sequencing
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                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Kirkpatrick
Canada's Michael Smith Genome Sciences Centre
BEC Cancer Agency
Suite 100, 570 West 7th Avenue, Vancouver, British Columbia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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/dev_stage="6 months old fetus"
/lab/bost="8. coli DH10B T1 Phage resistant"
/clone lib="GC BGG-29"
/note="Vector: pExpress 1; Site_1: Blunt (5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 27; DB 11; Length 110;
Pred. No. 1.3e+04;
0; Mismatches 45; Indels
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Plate: LB02989 row: P column: High quality sequence stop: 110.
Location/Qualifiers
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/clone="IMAGE:8486471"
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                                                                                                                                                                                                                                                                                                                                     Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 110)
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/strain="L1 Hereford"
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Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Canada, V5Z 456
TEL: 1-604-707-5900 x5406
Fax: 1-604-876-3561
                                                                                                                                       EE366986.1 GI:112227366
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Best Local Similarity 54.5%;
Matches 54; Conservative
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                                                                                                                                                                                                        Bos taurus (cattle)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2005)
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organism="Oryza sativa (indica cultivar-group)"
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Best Local S
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 22-JUN-2006
                                                                                                                                                                                                                                                                                                                                                       Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 TGTTTTCTGGATGCAGAGTCCTCTGACTCCCTCTGCCACGGGCTGAGTTTCCGGCTCCAG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1T283656_0934_2562 LNCAP + R1881 synthetic Androgen human prostate
                 Zambrowicz_B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, Bw. V. V., Kipp, P., Kohlhauff, B., Ma, Z.-O., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Shu, Q., Person, C. and Sands, A.T.
Whyl kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
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Mammalia; Eutheria; Buarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      British Columbia Genome Sciences Centre
Email: sjones@bcgsc.ca
EST was generated using 454 life sciences sequence-by-synthesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                            4000 Research Forest Drive, The Woodlands, TX 77381, USA Email: materials@lexgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 82;
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ENSG00000166548|ENST00000299697, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="OST122945"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 1295v/Ev"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 17;
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Pred. No. 2.1e+04;
0; Mismatches 33
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                                                                                                                                                                                                                                                                                             Lexicon Genetics Incorporated
                                                                                                                                                                                                                                                                                                                                                                                                Class: Gene Trap.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/strain="129Sv/Ev"
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                                                                                                                                                                                                                                                    Contact: Zambrowicz BP
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Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
Homo sapiens
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Best Local Similarity
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// note="INCaP human prostate cancer cells (American Type Culture Collection; Bethesda, MD) were maintained in RMH: 1640 media (StemCell Technologies; Vancouver, BC) supplemented with 10% fetal bovine serum (FBS; StemCell Technologies) and incubated at 37C with 5% CO2. Cells at passage 38 were plated at a density of approximately 4x10% cells per T175 flask, Cells were serum-starved for 48 hours prior to treatment for 16 hours with 10 nM R1881 (PerkinElmer; Woodbridge, Canada). Cells were harvested and total RNA was extracted from the cells using TRIZOL Reagent (Invitrogen Life Technologies, Carlsbad, CA) following the manufacturer's instructions"
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Hu, S., Zeng, C., Zhang, J., Zhang, Y., Li, R., Xu, Z., Li, S., Li, X.,
Zheng, H., Cong, L., Lin, L., Yin, J., Geng, J., Li, G., Shi, J., Liu, J.,
Li, H., Li, J., Wang, J., Deng, Y., Ran, L., Shi, X., Wang, X., Wang, X.,
Li, C., Ren, X., Wang, J., Wang, X., Li, D., Liu, D., Zhang, X., Ji, Z.,
Zhao, W., Sun, Y., Zhang, Z., Bao, J., Han, Y., Dong, L., Ji, J., Chen, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITICIGGATGCAGAGICCTCTGACTCCTCTGCCACGGGCTGAGTTTCCGGCTCCAGGT 125
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.ibrary Oryza sativa (indica cultivar-group) cDNA 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 TTGCCTGGCTGCCTCCTTCCTTGAGAGCTGTTCCCACCGCCTGCTCTTCCGGTTGGAGGC
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                                                                                                                     /clone lib="LNCAP + R1881 synthetic Androgen human prostate library"
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No.51 Zhijiang Road, Hangzhou 310008, China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 25.8; DB 11
Pred. No. 2.8e+04;
); Mismatches 32
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Seq primer: M13 Forward
High quality sequence stop: 110
POLYA=No.
                                                                     'tissue_type="prostate"
|cell_line="LNCap"
="taxon:9606"
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58.4%; Pred
0; P
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Wu, S. and Liu, J
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Best Local Similarity
Matches 48; Conserv
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DEFINITION
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EC536793
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KEYWORDS
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                 RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                         CL952591 110 bp DNA linear GSS 21-SEP-2004 OSIRUA001748 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
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                                                                                                                                                                                                                      186
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
1 (bases 1 to 110)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:39946"
/tissue_type="panicle"
/cell_type="sterile"
/dev_stage="heading/flowering"
/clone_lb="Oryza sativa cv. PA64s panicle sterile cDNA
library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Au.L., Wango,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Endang,X., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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/mol_type="genomic DNA"

/db_xref="texon:39946"

/clone lib="Gyyza sativa Express Library"

/note="Oryza sativa exon trapped genomic sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Oryza sativa (indica cultivar-group)"
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Pred. No. 2.8e+04;
0; Mismatches 27; Indels 0
                                                                                                                                                      Score 25.8; DB 9; Length 110;
Pred. No. 2.8e+04;
0; Mismatches 27; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (indica cultivar-group)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: chenchen@genomics.org.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
/mol_type="mRNA"
/cultivar="PA648"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CL952591.1 GI:52364600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genomic sequence.
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                                                                                                                                                      ch 10.2%;
1 Similarity 60.9%;
42; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Chen Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42; Conservative
                                                                                                                                                                                                                                                                               GAGACGAGC 195
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Best Local
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DEFINITION
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EST 25-APR-2006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biological Sciences
University of Southern California
3616 Trousdale Parkway #107, Mail Code 0371, Los Angeles, CA 90089,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST 22-JUN-2006
human prostate
                                                                                                                                                                                          Gillichthys mirabilis (long-jawed mudsucker)
Gillichthys mirabilis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopteryyii, Neopteryyii; Teleostei; Buteleostei; Neoteleostei;
Gobioidei; Gobiidae; Gillichthys.

[ bases 1 to 111)
BB652145

111 bp mRNA linear EST 25-APR-20 MNGSCLMHBHI03pTrip1Ex214j07f1 Gillichthys mixed tissue (liver, muscle, brain, heart, intestine) library 2 Gillichthys mirabilis cDNA clone 14j07 5', mRNA sequence.
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/tissue_type="Liver, muscle, brain, heart, intestine"
/dev stage="Adult"
/dab host="E.coli Electromax DH10B"
/clone_lib="Gillichthys mixed tissue (liver, muscle, brain, heart, intestine) library 2"
/note="vector: pTriplEx2; Site 1: Sfil GGCATTACGGCC; Site 2: Sfil GGCGCTCGGCC; Normalized and serially subtracted cDNA library prepared from environmentally challenged animals"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: gracey@usc.edu
Vector has been trimmed from this EST.
Plate: 14 row: j column: 07.
Seq primer: Triplex 5' LD (5'-CTCGGGAAGCGCCATTGTGTTGGT-3')
High quality sequence stop: 111.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EC536793 1175 LNCAP + 11881 synthetic Androgen 112646105 0517 1775 LNCAP + 11881 synthetic Androgen 11brary Homo sapiens CDNA similar to ENSG00000176095 ENST00000321599, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Gillichthys mirabilis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:822"
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                                                                                                                                                                                                                                                                                                                                                                                                       Gracey, A.Y.
Unpublished, Andrew Y. Gracey
Unpublished (2006)
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                                                                                                                                              EB652145.1 GI:93277671
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Fax: 213-740-8123
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Gaps

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63

source

FEATURES

GSS 05-OCT-2005

ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

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/note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI; He CHORI-243 sheep (M) (Ovis aries) BAC library produced by Pieter de nong's lab at CHORI thtp://bacpac.chori.org/library.php?id=162"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lauraeiatheria, Cetartiodactyla, Ruminantia,
Pecora, Bovidae, Caprinae, Ovis.
1 (bases 1 to 103)
                                                                                                                                               /organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="rcieg05m22"
/tissue_type="whole animal"
/dev_stage="egg"
/clone_lib="Nori Satoh unpublished cDNA library, egg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 bp DNA linear GSS 05-OCT 109847402684 CHORI-243 Ovis aries genomic clone CH243-202P18, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 301-795-7536
Email: ekirknessetigr.org
Sequences generated at the J. Craig Venter Institute Joint
Sequences generated at the J. Craig Venter Institute Joint
Technology Center (JCVIJTC; http://www.venterinstitute.org/).
Original Trace: 1098474026684 Trace TI: gnl[ti]918952333
Insert Length: 184000 Std Error: 0.00 row: P column: 18
Seg primer: SP6
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGCAACTGAGAGGGGTTAAGGCGTCCCCAAGTTGGAAGGGCGTTTGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Ewen Kirkness
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
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Ovine BAC End Sequences from Library CHORI-243
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                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                               Score 25.6; DB 7;
Pred. No. 3.2e+04;
0; Mismatches 19;
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satch@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="Texel breed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell_type="Blood"
/clone_lib="CHORI-243"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .103
/organism="Ovis aries"
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/clone="CH243-202P18"
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Other GSSs: 1098474028028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DU408432.1 GI:77138562
                                                                                                                                                                                                                                                                                                                                                                               ch 10.2%;
1 Similarity 66.1%;
37; Conservative
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Ovis aries
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Best Local Similarity
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                                                                   Catarrhini; Hominidae; Homo.

Catarrhini; Hominidae; Homo.

1 (bases 1 to 113)

Bainbridge, M.N., Warren, R.L., Hirst, M., Romanuik, T., Zeng, T.,

Go, A., Delany, A., Griffith, M., Hickenbotham, M., Magrini, V,

Mardis, B.R., Sadar, M.D., Siddiqui, A.S., Marra, M.A. and Jones, S.J.M.

Analysis of the prostate cancer cell line INCaP transcriptome using

a sequencing-by-synthesis approach

Unpublished (2006)
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1 (Dases 1 to 99)
Satou,Y., Kohara,Y. and Shin-i,T.
Expressed genes in Ciona intestinalis
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26
                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prostate library"
/note="LNCaP human prostate cancer cells (American Type
                                                                                                                                                                                                                                                                                                                                                                     Email: sjones@bcgsc.ca
EST was generated using 454 life sciences sequence-by-synthesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="prostate"
/cell_line="LNCaP"
/clone_lib="LNCAP + R1881 synthetic Androgen human
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                                                                                                                                                                                                                                                                                                                 Bioinformatics
British Columbia Genome Sciences Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Department of Zoology
Kyoto University
                                                                                                                                                                                                                                                                                            Contact: Steven Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 TTTCTGGATGCAGAGTC
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Query Match Best Local S: Matches 45,

ORIGIN

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Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Haplorrhini;
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citck, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
                                             TGTGTTCAAAATGCAGAATGAGAAATGTCACATTTCCCAGCTCTGGGTGACGGGGCCCGG
                   TGTTTTCTGGATGCAGAGTCCTCTGACTCCCTCTGCCACGGGCTGAGTTTCCGGCTCCAG
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/clone lib="ZM 0.7_1.5 KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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                                                                                       GTTCGCGTGTCGCCCTGAGGTTTGAGGC 151
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/strain="B73"
                                                                                                                       Geregegegegecregegegege
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                    CG255380.1 GI:34159750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 301-838-5843
Fax: 301-838-0208
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MR2-UM0060-170 Seq primer: puc 18 forward High quality sequence start: 9 High quality sequence start: 9 High quality sequence stop: 80.
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Groldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: uterus; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 GGCCAGACAGCTCGCAGTCGGGCAGGGGGGGGGGGGAGAGACGAGGGGGGCTCTGGCCCCT 208
                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 GGCCACACAACTCGCGAACTGGGTGGAGCTGAGGGTGGAAGGGGGAGTGGCACAGACCATC
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10737800
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llarity 55.8%; Pred. No. 4.1e+04;
Conservative 0; Mismatches 38;
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/organism="Homo sapiens"
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/dev_stage="Adult"
/clone_lib="UM0060"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                sequence tags
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Best Local Similarity
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AR166135 Sequence
AR235763 Sequence
AR235563 Sequence
AR279563 Sequence
AR899943 Sequence
BD0135476 Sequence
BD411059 An Oligon
BD411059 An Oligon
BD411330 OLIGONUCL
CQ540817 Sequence
A3044 Artificial
A3045 Artificial
A3045 Artificial
A3045 Artificial
BD461809 OLIGONUCL
CQ531296 Sequence
AX18312 Sequence
AX092132 Sequence
AX19312 Sequence
CQ001550 Sequence
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CQ001560 Sequence

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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Dickson, B., Berger, J., Suzuki, T. and Knoblich, J. Method for identifying therapeutic targets by use of screens in drosophila melanogaster Patent: WO 03042407-1A 200 22-MAY-2003; BOEHRINGER INGELHEIM INTERNATIONAL GMBH; CD Patents Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 49;
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DNA"
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51.5%; Pred. No. 2.5e+04;
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Sequence 200 from Patent WO03042407.
AX772410
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                                  AX899943
BD035476
AR735737
BD411059
BD471330
CQ540817
A30344
A30345
BD461809
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I11576
BD298221
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AX2138312
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CQ004542
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AR065689
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E08253.1 GI:2176374
JP 1994279497-A/12.
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Matches 17; Conservative
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BD464871 OLIGONUCL
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X14934 Mouse mpvv
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BD070385 Factor X-
AR340859 Sequence
AR118827 Sequence
CS254876 Sequence
AR126073 Sequence
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E08253 linker. 11/
AX898740 Sequence
BD0044273 Sequence
AR734534 Sequence
E08252 linker. 11/
                                                               June 19, 2007, 13:59:45; Search time 2184 Seconds (without alignments) 2500.230 Million cell updates/sec
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A86879 Sequence 19
BD070385 Factor X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                          ggagggcggggagagacga......ucucuccuuucgccaccucc
        GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd
                                                                                                                                                                                           3761712
                                                                                                                                                                       7568541 seqs, 34560148153 residues
                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                             nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AX772410
E08253
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BD034273
AR734534
E08252
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A86879
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AR118827
CS254876
AR126073
BD270121
BD464871
CQ534358
MWTRB138
HUMDYSTR
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AR031577 Sequence AR065689 Sequence AR097448 Sequence I49966 Sequence 16

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PAT 04-NOV-2005

PAT 27-AUG-2002

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ORGANISM

AUTHORS TITLE JOURNAL

COMMENT

REFERENCE

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C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
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                                                                                                                                                   Homo sapiens (human)
JP 2001269182-A/10519
02-OCT-2001
24-FEB-2000 JP 2000118773
25-FEB-1999 US 60/122487
JEAN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 51;
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                                linear
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1 (bases 1 to 51)

Edwards, J.-B.D.M., Duclert, A. and Giordano, J.-Y.

Expressed sequence tags and encoded human protei

Patent: US 6783961-A 14603 31-AUG-2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGAGGCGGGGGAGAGACGAGCGGCUCUGGCCCCUUAAUU 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47 GGGCGGCGGCGCAGCAGCGCTCAGGCCCCTGCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 19.2; DB 2;
Pred. No. 5.8e+04;
3; Mismatches 13;
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                              51 bp DNA tag and encoded human protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .51
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/organism="unknown"
/mol_type="genomic DNA"
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                                                                                     BD034273.1 GI:22576015
                                                                                                  JP 2001269182-A/10519.
Homo sapiens (human)
Homo sapiens
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24.3%;

Best Local Similarity 60.0%;

Matches 24; Conservative
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PC C12P2
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Haplorrhini,
                                                                                                                                                                                                             30-NOV-1990 JP 90P 335720, 25-PEB-1991 JP 91P 30271 PI TAKESHI, IWASAKI AKIO, SAINO SUKEYUKI, KIMURA SHIGERU, PI
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                                                                                                                                                                                                                                                                                                                                                                                                      /organism='Artificial sequences' Location/Qualifiers
   unidentified
unclassified sequences.
1 (bases 1 to 63)
Doi,T., Iwasaki,A., Saino,S., Kimura,S. and Oguchi,M.
THROMBIN-BINDING SUBSTANCE AND ITS PRODUCTION
Patent: JP 1994279497-A 12 04-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 24.3%; Score 19.2; DB 2; Length 51;
Best Local Similarity 60.0%; Pred. No. 5.8e+04;
Matches 24; Conservative 3; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47 GGCGGCGCGCAGCAGCGGCTCAGGCCCCTGCAGT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 25.1%; Score 19.8; DB 2; Score 19.8; Pred. No. 3.6e+04; 23; Conservative 4; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 bp DNi
Sequence 14603 from Patent EP1033401.
AX898740

    51
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

    .63
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

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04-OCT-1994
25-NOV-1991 JP 1991308976
3357...
1990 JP 90P 3357.
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                                                                                                                                          Artificial sequences.
JP 1994279497-A/12
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                                                                                                                                                                                                                                                                                                                                        topology: Linear;
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PC C07K13/0
C12P21/02,
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PAT 22-JAN-2000
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unclassified sequences.

1 (bases 1 to 39)
Himmelspach,M., Schlokat,U., Dorner,F., Andreas, Fisch and Bibl,J.
Factor X-analogues with modified procease cleavage site
Patent: JP 2001513631-A 19 04-SEP-2001;
BAXTER AG
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PN JP 2001513631-A/19
PD 04-SEP-2001
PP 74-FEB-1998 JP 1998537062
PR 27-FEB-1997 AT A 335/97
PI MICHELE HIMMELSPACH, UWE SCHLOKAT, FRIEDRICH DORNER, ANDREAS PI
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Himmelspach, M. and Eibl, J.
FACTOR X ANALOGUES WITH A MODIFIED PROTEASE CLEAVAGE SITE
PACTOR VO 9983317-A 19 03-SEP-1998;
HIMMELSPACH MICHELE (AT); EIBL JOHANN (AT)
Location/Qualifiers
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Factor X-analogues with modified protease cleavage site
BD070385
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                                                                                            24.1%; Score 19; DB 2; Length 65; 37.5%; Pred. No. 7.2e+04;
                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CCAGAATCGATTCTCGTGCTCGTTGTCGCCCCTCTC 39
                                                                                                                                                                                           40 UGUACTUCGGGCUCGUATUGUCTCCUCUCCUTUCGCCACCUCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 CCUDAAUGUACUUCGGGCUCGUAUUGUCUCCCUUUC
                                                                                                                                                                                                                                                                                                       DNA
                                                                                                                                 10; Mismatches
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

    .39
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    /db_xref="taxon:32644"

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Sequence 19 from Patent WO9838317.
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Strandedness: Single;
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Mammalia, Butheria, Buarchontoglires, Primates, Haplorhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                      25-NOV-1991 JP 1991308976
30-NOV-1990 JP 90P 335720, 25-FEB-1991 JP 91P 30271 PI
TAKESHI, IWASAKI AKIO, SAINO SUKEYUKI, KIMURA SHIGERU, PI
'HI MASAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Millennium Predictive Medicine, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                   Doi,T., Iwasaki,A., Saino,S., Kimura,S. and Oguchi,M. THROMBIN-BINDING SUBSTANCE AND ITS PRODUCTION Patent: JP 1994279497-A 11 04-OCT-1994;
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                                    œ
 1 GGAGGGCGGGGGAGACGAGCGGCUCUGGCCCCUUAAUU
                     47 GGCGGCGGCGCGCAGCAGCGGCTCAGGCCCCTGCAGT
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                                                                                                                                   DNA
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    .65
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

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Sequence 271 from Patent WO0142467.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     strandedness: Single;
                                                                                                                                                                                                                                                                                                                                                                                              Artificial sequences.
JP 1994279497-A/11
04-OCT-1994
                                                                                                                                                                                   E08252.1 GI:2176373
JP 1994279497-A/11.
unidentified
unidentified
unclassified sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        topology: Linear;
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Best Local Similarity 62.9%;
Matches 22; Conservative
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OGUCHI MASAC
CI12P21/02,
PC (CI2NI,
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PAT 16-MAY-2001
                                                                                                     PAT 01-FEB-2006
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Saccharomyces cerevisiae
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetales;
                                                                                                                                                                                                                                                                                    isoprenoid pathways
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Janjic, N., Gold, L. and Tasset, D.
High affinity ligands of basic fibroblast growth factor and
   54 GGGGGGGGGGGGGTTCTATAGTGTCACCTAAATCGTATGGCGGCGGCGAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                   Kuehnle, A.R. and Hahn, F.M.
Manipulation of genes of the mevalonate and isopre create novel traits in transgenic organisms
Patent: WO 2002010398-A 15 07-FEB-2002;
Kuehnle, Adelheid R. (US); Hahn, Frederick M. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                  /organism="Gaccharomyces cerevisiae"
/mol_type="unassigned DNA"
/db_xref="taxon:4932"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 23.8%; Score 18.8; DB 2; Scinilarity 38.7%; Pred. No. 8.8e+04; 24; Conservative 11; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.8%; Score 18.8; DB 2; 28.3%; Pred. No. 8.7e+04; ive 16; Mismatches 17;
                                                                                                Sequence 15 from Patent WO2002010398.
CS254876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent: US 6177557-A 415 23-JAN-2001;
Location/Qualifiers
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Sequence, 415 from patent US 6177557.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="unknown"
/mol_type="unassigned DNA"
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BD270121/c
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CS254876/c
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Himmelspach, M., Schlokat, U., Dorner, F., Fisch, A. and Eibl, J.
Factor X analogues with a modified protease cleavage site
Patent: US 6573071-A 19 03-UUN-2003;
Baxter Aktiengesellschaft; Vienna;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 GGCGGGGGAGAGAGGGGCGCCCCTUAAUUGUACUUCGGGCUCGUAUU
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larity 44.7%; Pred. No. 7.9e+04;
Conservative 9; Mismatches 12; Indels
                                                                                                                                            Score 18.8; DB 2; Length 39;
Pred. No. 7.9e+04;
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/organism='Unidentified'
Location/Qualifiers
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illarity 48.1%; Pred. No. 8.3e+04;
Conservative 6; Mismatches 22;
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Sequence 753 from patent US 6150087.
                                                                                                                                                                                                                                                                                                                     39 bp 1
Sequence 19 from patent US 6573071.
AR340859
AR340859.1 GI:33732706
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/wol_type="unassigned DNA"
                                                                                                                                                                              9; Mismatches
                                                            organism="unidentified"
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/db_xref="taxon:32644"
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Chien, D.Y.
NANBV diagnostics and vaccines
Patent: US 6150087-A, 753 21-NON
Location/Qualifiers
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                                                                                                                                            23.8%;
                                                                                                                                                                              17; Conservative
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Best Local Similarity
Matches 26; Conserva
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Unclassified.
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17; Conserv
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Best Local Similarity
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Query Match Best_Local Matches 1

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   BD270121 55 bp DNA linear PAT 04-NOV-2005
Method of screening antiamyloid development properties and method
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                                                                                                                                              other sequences; artificial sequences.

1 (bases 1 to 55)
Masliah,E., Hashimoto,M. and Rocknstein,E.
Machod of screening antiamyloid development properties and method of treating neurodegenerative diseases
Patent: JP 2002538076-A 3 12-NOV-2002;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                     .47-01.05/09,C12N15/00
C12N15/09,C12N15/00
encoding amino acids 73-83 of human NACP/alpha-synuclein and
amino acids
73-79 of human beta-synuclein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 65)
Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.
OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
VARIANTS THAT POPULATE A TRANSCRIPTOME
Patent: JP 2004508019-A 3993 18-MAR-2004;
Avi SHOSHAN, Alon WASSERMAN, Eli MINTZ, Liat MINTZ, Simchon FAIGLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JUL-2001 JP 2002516365
02-MAY-2001 US 60/287724,28-JUL-2000 US 60/221607 PI
Shoshan,alon wasserman,eli mintz,liat mintz,simchon PI
                                                                                                                                                                                                                                                                                                                                                                       ELIEZER MASLIAH, MAKOTO HASHIMOTO, EDWARD ROCKNSTEIN PC
15/00, A61P25/16, A61P25/28, A61P43/00, C12Q1/02, G01N33/15, PC
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Pred. No. 9.9e+04;
9; Mismatches 19

    .55
    forganism="synthetic construct"
|mol_type="unassigned DNA"
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                                         treating neurodegenerative diseases
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06-OCT-1998 US 60/103310
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JP 2004508019-A/3993
                                                                                                                                                                                                                                                                              Artificial Sequence
JP 2002538076-A/3
                                                                          GI:33079889
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JP 2004508019-A/3993.
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Best Local Similarity 42.9
Matches 21; Conservative
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Best Local Similarity 63.6%; Pred. No. 1e+05;
Matches 21; Conservative 3; Mismatches
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    .65
    /organism="unidentified"
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                                                                                                                                                                                                                                                                   40 AGCCTGAGGACAGAGAGTGGCTCTGCCCCAT
  Location/Qualifiers
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ALIGNMENTS

ABK15487

Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Post-processing:

Geneseq 200701:* geneseqn1980s:* geneseqn1990s:*

Database

Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss. Human secreted protein 5' EST, SEQ ID NO: 14603 Duclert A, Giordano J; BP 21-FEB-2000; 2000EP-00200610. 99US-0122487P. RESULT 1 AAC10528/c ID AAC10528 standard; cDNA; 51 06-OCT-2000 (first entry) Dumas Milne Edwards J, (GEST) GENSET. 26-PEB-1999; Homo sapiens EP1033401-A2 06-SEP-2000. AAC10528;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2005s:* geneseqn2006s:* geneseqn2007s:*

geneseqn2003ds:* geneseqn2004as:* qeneseqn2003cs:*

geneseqn2003as:* geneseqn2003bs:*

geneseqn2004bs:*

SUMMARIES

WPI; 2000-500381/45.

Aad31044 Oligonucl Aaf70953 bFGF DNA Aat00367 Family 4 Aaa09070 Sense pri Abn31245 Rat splic

AAD31044 AAF70953 AAT00367 AAA09070 ABN31245 AEG84737

22233333888

4 2 9 7 8 6 5

AAV56769 AAD30987

AAC10528

В

Query Match Length

Result Š. ADM95117 AEH27179

AAX59388

15 12 13 13 15 15 15

AAC11731 ADP49484 AEL27903

m. m. 0

Aac10528 Human sec Adm79864 DNA ligan

Description

Aah68997 Human cer Aav56769 Human Fac Aad30987 Schizosac

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.

Claim 1; SEQ ID NO 14603; 71pp + Sequence Listing; English.

The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR)

	GenCore version 6.2.1 Copyright (c) 1993 - 2007 Biocceleration Ltd.
OM nucleic - nuc	OM nucleic - nucleic search, using sw model
Run on:	June 19, 2007, 13:52:37 ; Search time 314 Seconds (without alignments) 1864.442 Million cell updates/sec
Title: Perfect score: Sequence:	US-10-604-726A-5135 79 1 ggagggggggggagacgaucucuccuuucgccaccucc 79
Scoring table:	IDENTITY NUC Gapop 10.0 , Gapext 1.0
Searched:	5620219 seqs, 3705283702 residues
Total number of	Total number of hits satisfying chosen parameters: 6021484
Minimum DB seq length: 0 Maximum DB seq length: 8(ength: 0 ength: 80

genesequ2000s:* genesequ2001as:* genesequ2001bs:* genesequ2002as:* genesequ2002bs:*

Aax59388 Saccharom Aac11731 Human sec Adp49484 Oligonucl Ae127903 Primer fo

Aeg84737 Hematolog Adm95117 Rat antis Aeh27179 Human acu

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This invention relates to a novel method (CE-SELEX, Capillary Electrophoresis-Systematic Evolution of Ligands by Exponential enrichment) of identifying nucleic acid Ligands of a target molecule from a candidate mixture comprised of single stranded nucleic acids each having a region of randomised sequence by contacting the mixture with the target molecule, where nucleic acids having affinity to the target molecule are partitioned from the mixture by capillary electrophoresis, amplifying increased affinity nucleic acids to yield a ligand-enriched mixture of nucleic acids. The invention may be useful for the production of compounds with an antiasthmatic, cerebroprotective, anti-HIV or
of the mRNA because they are often obtained from oligo-dT primed cDNA ibbraries. Such ESTs are not well suited for isolating CDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length CDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying nucleic acid ligand of target molecule from mixture comprising single stranded nucleic acids having region of randomized sequence by contacting mixture with target molecule, amplifying affinity
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CE-SELEX; capillary electrophoresis; ligand-enriched mixture; antiasthmatic; cerebroprotective; anti-HIV; virucide; analytical chemistry; in vivo imaging; biosensor; complex matrix; affinity probe capillary electrophoresis; APCE; ELISA; fibre-optic microarray biosensor; histological marker; tumour microvessel; anthrax spore; cocaine; de.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA ligand identification-related aptamer DNA sequence SeqID6.
                                                                                                                                                                                                                                                          Query Match 24.3%; Score 19.2; DB 3; Length 51; Best Local Similarity 60.0%; Pred. No. 7.4e+03; Matches 24; Conservative 3; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                  GGAGGCGGGGAGAGACGAGCGGCUCUGGCCCCUUAAUU 40
                                                                                                                                                                                                                     Sequence 51 BP; 5 A; 23 C; 19 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                     GGGCGGCGCGCGCAGCGGCTCAGGCCCCTGCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID NO 6; 90pp; English.
                                                                                                                                                                             expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADM79864 standard; DNA; 80 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAY-2002; 2002US-0384709P.
15-MAY-2003; 2003US-0470750P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MINU ) UNIV MINNESOTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADM79864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
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                                                                                                                                            research: Improved appeared are usered. In Gueraching unage, in vivo imaging and blosensors. The aptemers are also useful in quantitating targets apreases are used to develop high-present in complex matrices. The aptemers are used to develop high-sensitivity affinity probe capillary electrophoresis (APCE) assays, in ELISA type assays using enzyme-linked DNA aptemers. Thrombin aptemers may be developed for using fibre-optic microarray biosensors. Aptemers may histological markers to identify tumour microvessels. Aptemers may be developed for use in other aptemer-based assays, such as assays for analytes ranging from anthrax spores to cocaine. Aptemers having improved quality, improved binding efficiency and selectivity can be identified by the method of the invention. The present sequence is that of an aptemer DNA sequence which was identified using the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer.
virucide activity. The method is useful for identifying nucleic acid ligands of a target molecule from a candidate mixture comprised of single stranded nucleic acids each having a region of randomised sequence. Aptamers identified by the method are useful as a tool in analytical chemistry, useful in wide range of diagnostic assays and as direct benefits to many area of the research, including biomedical and health research. Improved aptamers are useful in developing diagnostic assays,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 GCGGGGGAGAGAGGACGACCGCUUGGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUCUC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ecaecacadadercadaretrereracerrarrirerecercadeareceregerrane 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 24.3%; Score 19.2; DB 12; Length 80; Best Local Similarity 35.9%; Pred. No. 8e+03; Matches 23; Conservative 13; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 80 BP; 17 A; 21 C; 21 G; 21 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cervical cancer marker nucleic acid 271.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhao X;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH68997 standard; cDNA; 65 BP
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12-MAY-2000; 2000US-0203791P
09-UUN-2000; 2000US-0210600P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 CUUU 69
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                                   cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition, to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be
                  invention relates to novel genes (AAH68727-AAH73383) associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Factor X; analogue; activation cleavage site; protease; bleeding; human; defect; Factor IX; Factor VII; Factor VIII; haemophilia; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New factor X analogues with processing site for protease not active on natural protein - and related DNA, is very stable and can be activated virto or in vivo without using animal protease(s), particularly for treating disorders of blood coagulation.
                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                 15; Indels
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                                                                                                                                                                                                                                                                                                                        40 UGUACUUCGGGCUCGUAUUGUCUCCUUUCGCCACCUCC 79
                                                                                                                                                                                                   Sequence 65 BP; 19 A; 17 C; 19 G; 4 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                               TTTTCTTCGTCNTCGAANANTCTCTTCCTTCGCTNNCGCC
                                                                                                                                                                                                                                                                                 10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Factor X PCR primer #1017.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV56769 standard; DNA; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                 15; Conservative
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                                                                                                                                                                                                                                                              Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR primer; ss
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CCC 6769
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plants and microalgae, ror providing transformed cells, and for providing a cell with an inserted polymucleotide sequence encoding one or more products of interest. The present sequence is a PCR primer used to inchinancharomyces nombe IPP isomerase encoding orf. This primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to the use of specific genes of the mevalonate an isoprenoid biosynthetic pathways and inactive gene sites (pseudogene). Genes of the invention are used to enhance biosynthesis of isopentenyl diphosphate (IPP), dimethylallyl diphosphate (DMAPP) and isoprenoid pathway derived products in the plastids of transgenic plants and microalgae, for producing herbicide or antibiotic resistant transgenic plants and microalgae, for providing transformed cells with increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe IPP isomerase encoding orf sense PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mevalonate; isopentenyl diphosphate; herbicide resistance; DMAPP; IPP isoprenoid; dimethylallyl diphosphate; antibiotic resistance; enzyme; transgenic plant; IPP isomerase; PCR primer; ss.
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activation. Activated analogues have good stability and structur; integrity and are practically free of inactive intermediates and autoproteolytic decomposition products
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                                                                                                                   Length 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isolate Schizosaccharomyces pombe IPP isomerase encoding is used in the exemplification of the invention
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                                                                             U; 0 Other;
                                                                                                                                                                                                                      2 CCAGAATCGATTCTCGTCGTCGTCGTCGCCCCTCTC 39
                                                                                                                                                                                              33 CCUUAAUUGUACUUCGGCUCGUAUUGUCUCUCCUUUC
                                                                                                                 23.8%; Score 18.8; DB 2; ilarity 44.7%; Pred. No. 9.7e+03; Conservative 9; Mismatches 12
                                                                             Sequence 39 BP; 5 A; 14 C; 8 G; 12 T; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JUL-2000; 2000US-0221703P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-217122/27.
                                                                                                                                     Best Local Similarity
Matches 17; Conserv
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Best Local Similarity
Matches 13; Conserv
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                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                              RESULT 5
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AAV56751-V56775 are primers used in a method resulting in the production of novel human Factor X (F10) analoques. Such analoques have in the region of the natural F10a activation cleavage site, a modification that creates a processing site for a protease that does not naturally cleave F10 in this region. The proteins are used to generate, in vivo or in viro, F10a analogues that can be used to control bleeding and for treating defects of factors IX, VII or VIII, e.g.in haemophiliacs who acid can be used in gene therapy of the same conditions. The analogues have developed antibodies to factors VIII and/or IX. The encoding nucleic acid can be used in gene therapy of the same conditions. The analogues have high stability and can be activated without use of animal enzymes such as trypsin. Only activation is affected, their activity is the same as the natural factor. The analogues can be isolated as a pure singlecthain pro-protein (not usually possible because of rapid processing of the native precursor) and this converted to two-chain form by subsequent

72 CCTTAATTGTTCTTCATCATAATCCTTTTTCTCTTTGTTGGGAACTC 27

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The invention relates to the use of specific genes of the mevalonate and isoprenoid biosynthetic pathways and inactive gene sites (pseudogene). Genes of the invention are used to enhance biosynthesis of isopentenyl diphosphate (IPP), dimethylallyl diphosphate (DWAPP) and isoprenoid pathway derived products in the plastids of transgenic plants and microalgae, for producing herbicide or antibiotic resistant transgenic plants and microalgae, for providing transformed cells with increased isoprenoid production compared to non-transformed cells, and for providing a cell with an inserted polymucleotide sequence encoding one or more products of interest. The present sequence is an oligomorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of specific genes of mevalonate and isoprenoid biosynthetic pathways, for providing a cell with herbicide or antibiotic resistance, and for
                                                                                                                                                             Mevalonate; isopentenyl diphosphate; herbicide resistance; DMAPP; IPP; isoprenoid; dimethylallyl diphosphate; antibiotic resistance; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        containing Saccharomyces cerevisiae DNA. This oligo is related to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for providing a cell with herbicide or antibiotic resistance, and f
providing transformed cells having increased isoprenoid production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.8%; Score 18.8; DB 6; Length 72;
28.3%; Pred. No. 1.1e+04;
                                                                                                                                Oligonucleotide #2 containing Saccharomyces cerevisiae DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 CCUDAAUUGUACUUCGGGCUCGUAUUGUCUCUCCUUUCGCCACCUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 72 BP; 30 A; 10 C; 18 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 99; 193pp; English.
                                                                                                                                                                                                                                                                                                                                                                    31-JUL-2001; 2001WO-US024037
                                                                                                                                                                                                                                                                                                                                                                                                   31-JUL-2000; 2000US-0221703P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF70953 standard; DNA; 79
                               AAD31044 standard; DNA; 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Conservative
                                                                                                                                                                                                                                Saccharomyces cerevisiae.
Unidentified.
Chimeric.
                                                                                                                                                                                                   transgenic plant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hahn FM, Kuehnle AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    KUEHNLE A R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-217122/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    (HAHN/) HAHN F M.
                                                                                                                                                                                                                                                                                                  WO200210398-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-APR-2001
                                                                                               31-MAY-2002
                                                                                                                                                                                                                                                                                                                                   37-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF70953;
                                                              AAD31044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KUEH/)
                 AAD31044/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
RESULT
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16; Mismatches 17; Indels

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The present invention relates to a purified and isolated non-naturally occurring DNA ligands to basic fibroblast growth factor (bFGF). The ligands are useful as part of gene therapy treatments and for diagnosing pathogenesis of vascular diseases including initiation and progression of atherosclerosis, acute coronary syndromes, vein graft disease and restanosis following coronary syndromes, the ligands have improved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 ACGAGCGGCUCUGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUCUCCUUUCGCCACC
                                                                                                                                                                                                                                                                                                                               Novel nucleic acid ligands to basic fibroblast growth factor that are useful as inhibitors of basic fibroblast growth factors and 2'-amino modified RNA ligands, exhibit increased in vivo stability.
                                    Ligand; basic fibroblast growth factor; bFGF; gene therapy; vascular; atherosclerosis; angioplasty; stability; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Family 1; family 2; ligand; thrombin;
systematic evolution of ligands.by exponential enrichment; SELEX;
heparin; selection; region of homology; inhibitor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.8%; Score 18.8; DB 4; Length 79; 38.7%; Pred. No. 1.1e+04; ive 11; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 79 BP; 18 A; 25 C; 13 G; 23 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Family 4 bFGF DNA ligand bl0 (experiment 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Col 69-75; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                   Tasset D;
                                                                                                                                                                              90US-00536428
91US-00714131
                                                                                                                                                     96US-00687421
                                                                                                                                                                                                       92US-00973333
                                                                                                                                                                                                                                94US-00219012
                                                                                                                                                                                                                    94US-00195005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT00367 standard; DNA; 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                          (NEXS-) NEXSTAR PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                           WPI; 2001-158583/16.
            DNA ligand #86.
                                                                                                                                                                                                                                                                                   Gold L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stability in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-AUG-1996
                                                                                                                                                    05-AUG-1996;
                                                                                                    US6177557-B1
                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 UC
                                                                                                                                                                                                                                28-MAR-1994;
                                                                                                                            23-JAN-2001.
                                                                                                                                                                               11-JUN-11990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24;
                                                                                                                                                                                           10-JUN-1991
06-NOV-1992
                                                                                                                                                                                                                    10-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT00367;
                                                                                                                                                                                                                                                                                   Janjic N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
             PFGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
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NACP/alpha-synuclein; beta-synuclein; beta-synuclein delta 1; mutz primer; neurodegenerative; Alzheimers disease; Parkinsons disease;

body disease; ss

Lewy Homo

sapiens

Synthetic

Sense primer for PROEX-1-beta-synuclein delta 1 construction.

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fibroblast growth factor (bEGF). These sequences were isolated using the primers and target regions given in AAQ98421-29 using systematic evolution of ligands by exponential enrichment (SELEX). DNA templates containing a region of 30 or 40 random nucleotides flanked by constant sequence regions, were synthesized. The constant regions were designed to be amplified by the primer. The primer 197.185 has 2 biotin phosphoramidites and two additional A residues covalently attached to its 5' terminus during synthesis. The random region was generated by utilising an equinolar mixture of the four nucleotides during oligonic encloses. Three pools of ssDNA were created that contain internal random regions. Each pool was incubated with bFGF at an excess of DNA to target. DNA bound to bFGF were selected by filtration. The selected single stranded DNA (sebNA) was then amplified by PCR. A significant improvement in affinity of DNA ligands was seen after 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identification of ligands to basic fibroblast growth factor and thrombin - which can be modified for increased in vivo stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rounds of selection. Five distinct families of ssDNA were identified, based on regions of homology. Some sequences showed no obvious homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequences given in AAT00282-394 represent DNA ligands to basic
                                                                                                                                                         /*tag= d
/note= "given in the specification as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to the five families and are considered to be orphans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 80 BP; 18 A; 25 C; 13 G; 23 T; 0 U; 1 Other;
                                                /*tag= b
/note= "Variable region"
/*tag= a
/note= "Fixed region"
                                                                                                    /*tag= c
/note= "Fixed region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 21; Page 108; 236pp; English.
                                                                                                                                                                                                                                                                                                                94US-00195005.
                                                                                                                                                                                                                                                                                95WO-US001458
                                                                                                                                                                                                                                                                                                                                                                    (NEXS-) NEXSTAR PHARM INC
                                                                                    .80
                                1. .58
                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-293073/38
                                                                                                                                                                                                                                                                                                                                                                                                       Gold L,
                                                                                                                                       misc_difference
                                    misc_feature
                                                                                    misc_feature
                                                                                                                                                                                                                                                                                06-FEB-1995;
                                                                                                                                                                                                                                                                                                                  10-FEB-1994;
                                                                                                                                                                                                                                                                                                                                    28-MAR-1994;
                                                                                                                                                                                                           WO9521853-A1
                                                                                                                                                                                                                                             17-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                        Janjic N,
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17 ACGAGCGGCUCUGGCCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUCUCCCUUCGCCACC 76
                                                                                                                7 ACGATCTGACTAGCCACCTGCATAGGAGTACCGATTGTATGTCACCTAGCTTAC 66
                                                      Gaps
    23.8%; Score 18.8; DB 2; Length 80; ilarity 38.7%; Pred. No. 1.1e+04; Conservative 11; Mismatches 27; Indels
Query Match
Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                  :-
TC 68
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(first entry)

10-AUG-2000

AAA09070;

AAA09070 standard; DNA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and treatment of, neurodegenerative disease. The methods comprise measuring aggregation of neurons of NACP/alpha-synuclein and stimulating expression of a non-amyloidogenic protein in order to reduce the level of aggregation. In the screening method, oxidative stress is stimulated in the neuronal cells by introduction of metal ions and hydrogen peroxide. The methods are useful for treating and screening treatments for neurodegenerative disease consisting of Alzheimer's disease, Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                         Screening treatments for neurodegenerative disease, such as Alzheimer's disease, comprises stimulating oxidative stress and measuring and aggregation of non-amyloid beta component /alpha-synuclein in neuronal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat spliced transcript detection oligonucleotide SEQ ID NO:3993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18.6; DB 3; Length 55;
Pred. No. 1.2e+04;
9; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 CGAGCGCCUCUGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUCUCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, mouse, rat, splice transcript, detection, RNA transdeppice variant, transcriptome, oligonucleotide library; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 55 BP; 16 A; 11 C; 23 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 45; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease and Lewy body disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.5%;
ilarity 42.9%;
Conservative 9
                                                                                                                                                                                                                                       99WO-US023134
                                                                                                                                                                                                                                                                         98US-0103310P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                        (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-303637/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                     WO200020020-A2.
                                                                                                                                                                                                                                       06-OCT-1999;
                                                                                                                                                                                                                                                                         06-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-2002
                                                                                                                                                                                                      13-APR-2000
                                                                                                                                                                                                                                                                                                                                          Masliah E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABN31245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49
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07-FEB-2002

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The invention relates to a system for profiling hematological cancer, comprises polynucleotide probes comprising a sequence corresponding to, comprises polynucleotide probes comprising a sequence corresponding to, compulementary to, an mRNA transcribed from candidate genes whose expression pattern is indicative of one or more feature of a hematological cancer chosen from lymphoma and leukemia. The hematological cancer chosen from lymphoma and leukemia. The hematological cancer is a lymphoma chosen from lymphoma, splenic marginal zone B-cell lymphoma, nodal marginal zone B-cell lymphoma, cell myeloma/plasmacytoma, FL, MCL, Burkitt's lymphoma, DLBCL, Hodgkin's lymphoma, lympholastic
Clymphoma, ALCL, cutaneous T-cell lymphoma, myeloma/plasmacytoma, respincemental T-cell lymphoma, intestinal T-cell
Clymphoma, and adult T-cell lymphoma), intestinal T-cell
Clymphoma, and adult T-cell lymphoma, intestinal T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                   System for profiling hematological cancer, comprises probes complementary to mRNA transcribed from candidate genes whose expression pattern is indicative of a feature of the cancer e.g. MYH11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a leukemia chosen from acute myelogenous leukemia, acute lymphocytic leukemia, chronic myelogenous leukemia, and chronic lymphocytic leukemia. The system is useful for the preparation of a nucleic acid array. The system enables accurate diagnosis and risk assessment of the hematological cancer. The present sequence represents a hematological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat; antisense oligonucleotide; ss; antisense RNA production; oncogenes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 GAGACGAGCGCCUCUGGCCCCCUUAAUUGUACUUCGGGCUCGUAIUGGUCUCCUCTUUC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.5%; Score 18.6; DB 15; Length 70;
40.4%; Pred. No. 1.3e+04;
Live 10; Mismatches 24; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 70 BP; 14 A; 21 C; 17 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumour suppressor; cell cycle regulator; ion channel
transport protein; intracellular signal transduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; SEQ ID NO 4293; 356pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hematological cancer. The present ecancer profiling, HCP, 70mer probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat antisense oligonucleotide #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADM95117 standard; DNA; 80 BP
                                                                                                                                                    27-SEP-2005; 2005WO-CA001464.
                                                                                                                                                                                                                27-SEP-2004; 2004US-0613980P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23; Conservative
                                                                                                                                                                                                                                                                           (MEDB-) MED BIOGENE INC.
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2006-293215/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                               WO2006034573-A1.
                                                                                                                                                                                                                                                                                                                                    Yoganathan T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-2004
                                                                                        06-APR-2006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADM95117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADM95117,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           messenger RNAs that populate a (sub-)transcriptome, where the (sub-
) transcriptome comprises messenger RNAs transcribed from multiple
transcription units that populate a genome. The library comprises several
oligonucleotides, each capable of hybridising selectively to a set of
messenger RNAs transcribed from a given transcription unit of the genome,
which encodes one or more messenger RNA splice variants. The
oligonucleotide libraries are useful for detecting mRNAs from a
biological sample, in expression profiling studies, in qualitatively or
can sample transcripts and splice variants of human or animal
transcriptomes. The libraries may also be used as specialised min
clibraries to detect transcripts of a sub-transcriptome under a particular
biological or pathological state, and so allowing the detection of tissue
and pathology-specific genes such as those genes only expressed in
specific tissue under a specific pathological condition; to detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          developmental specific genes, and to defect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27233 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of genome, useful for detecting tissue-, pathology-, and developmental-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes oligonucleotide libraries for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 directly from WIPO at ftp.wipo.int/pub/published pct sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.5%; Score 18.6; DB 6; Length 65; 63.6%; Pred. No. 1.2e+04; ive 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      Faigler S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 65 BP; 13 A; 21 C; 19 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 AGGCCGGGGAGAGACGAGCGGCUCUGGCCCCTU 35
                                                                                                                                                                                                                                                                                                                                                                                                Mintz E, Mintz L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 Agccrdasgasasasasasascrcrdccccar 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; SEQ ID NO 3993; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AEG84737 standard; DNA; 70 BP
                                                                                                                                                                                   20-JUL-2001; 2001WO-IB001903.
                                                                                                                                                                                                                                            28-JUL-2000; 2000US-0221607P.
02-MAY-2001; 2001US-0287724P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   Shoshan A, Wasserman A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 63.6
nes 21; Conservative
                                                                                                                                                                                                                                                                                                                                       (COMP-) COMPUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-257383/30.
      Rattus norvegicus.
                                                               WO200210449-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specific genes
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Gaps

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cell-cell communication protein; stress response gene; apoptosis related gene; growth factor; chemokine; interleukin; interferon; hormone; neurotransmitter; cell surface antigen; cell adhesion molecule.

cancer; cytostatic; neoplasm; lymphoma; leukemia; DNA array; diagnosis;

Homo sapiens

ss; probe.

Hematological cancer profiling, HCP, 70mer probe SEQ ID NO 4293.

01-JUN-2006

SXXXXXXXXXXXXXX

AEG84737;

RESULT 11 AEG84737

Query Match Best Loc Matches

ò q transcription factor; DNA-binding protein;

channel protein;

15-APR-2004

Rattus sp.

Chenchik A;

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The invention relates to a method of identifying an individual having altered risk of or susceptibility for developing acute myocardial infarction (AMI) which comprises providing blological sample of individual, collecting personal and clinical information, determining nucleotides present in polymorphic sites of single nucleotide or underday associated with AMI, and combining single SNP markers data with personal and clinical information. The method is useful for identifying an individual having an altered risk of or susceptibility for developing susceptibility or predisposition to AMI in an individual. The method is useful for identifying compounds useful in prevention or treatment of coronary heart disease (CHD) such as AMI. The method is useful for preventing or treating CHD such as AMI. The method is useful for diagnosing a human subject suffering from CHD such as AMI. The present suseful for diagnosing a subtype of AMI in an individual having AMI. The present sequence represents a human acute myocardial infarction (AMI) single not form part of the printed specification, but was obtained in the form the form part of the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying individual having altered risk of or susceptibility to develop acute myocardial infarction (AMI), comprises determining polymorphisms in AMI risk genes and combining polymorphisms data with personal and clinical information.
                                                                                                                                                                                                                                                                                                                                                                                             Salonen JT, Aalto J, Fuentes R, Kontkanen O, Pirskanen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.3%; Score 18.4; DB 15; Length 51; 41.3%; Pred. No. 1.4e+04; tive 10; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 CCCUDANUGUACUUCGGGCUCGUAUUGUCUCCCUUUCGCCACCU 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/note= "Single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 51 BP; 9 A; 16 C; 8 G; 17 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 1090; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                     15-OCT-2004; 2004FI-00001340.
03-JUN-2005; 2005US-00143642.
                                                                                                                                                                                                 12-OCT-2005; 2005WO-FI050355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ilarity 41.3%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX59388 standard; DNA; 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                         (JURI-) JURILAB LTD OY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2006-331490/34.
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les 19; Conserv
                                                                                   WO2006040409-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-SEP-1999
                                                                                                                                          20-APR-2006
                                                                                                                                                                                                                                                                                                                                                                                                                             Uimari P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX59388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a standardising control for RNA samples to be tested on non-control gene sequences on nucleic acid arrays, comprising a pool of unique tagged synthetic antisense mRNA molecules of a known concentration, where any two sequences are unique if their sequences differ. The non-control gene sequences on the nucleic acid array comprise oncogenes, genes encoding tumour suppressors, cell cycle regulators, ion channel proteins, transport proteins, intracellular signal transduction modulator and effector factors, transcription factors, DNA-binding proteins, receptors or cell-cell communication proteins, stress response genes, apoptosis related genes, DNA synthesis/recombination/repair genes and DNA-binding proteins. The genes encoding receptors comprise receptors for growth factors, chemokines, interleukins, interferons, hormones, neurotransmitters, cell surface antigens or cell adhesion molecules. The genes encoding cell-cell communication proteins comprise growth factors, chemokines, interleukins, interferons or hormones. The genes encoding cell-cell communication proteins comprise growth factors, cytokines, chemokines, interleukins, interferons or hormones. The genes encoding cell-cell communication proteins comprise growth factors, cytokines, chemokines, interleukins, interferons or hormones. The sequences on nucleic acid arrays is useful for producing a population of distinct antisense RNA molecules from an initial population of distinct antisense RNA molecules from an initial population of machine the sequences of the second arrays is useful for producing an antisense oligonucleotide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                    New standardizing control for RNA samples to be tested on non-control gene sequences on nucleic acid arrays, useful for producing a population of distinct antisense RNA molecules from an initial population of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myocardial infarction; cardiant; cardiovascular disease;
single nuclectide polymorphism; SNP; diagnosis; coronary artery disease;
vasotropic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 GGGAGAGAGGAGGGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUCCC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 18.6; DB 12; Length 80;
Pred. No. 1.3e+04;
8; Mismatches 24; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 80 BP; 18 A; 30 C; 16 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human acute myocardial infarction SNP SEQ ID NO 1090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 10; 282pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEH27179 standard; DNA; 51 BP
                                                                                                                                                                       07-MAR-2003; 2003US-00384245.
                                                                                                                                                                                                                              07-MAR-2002; 2002US-0362823P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 23.5%;
l Similarity 43.9%;
25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          distinct mRNA molecules.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-373913/35.
                                                                                                                                                                                                                                                                                  (CHEN/) CHENCHIK A.
                                                            US2004072191-A1
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Gaps

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D9798.4; AN97 homologue; essential gene; fungicide; fungistatic; anti-yeast; screening; infection; therapy; PCR; primer; ss.

Location/Qualifiers

Homo sapiens

Key variation

15-JUN-2006

AEH27179;

RESULT 13

g

Matches

Saccharomyces cerevisiae essential gene D9798.4 PCR primer.

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this patent did

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The present sequence is one of a large number of 5' ESTS derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTS are derived from mRNAs with intect 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. S' ESTS are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                      New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                             Claim 1; SEQ ID NO 15806; 71pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 65 BP; 12 A; 15 C; 26 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 gcggggagagacgagcggcucuggccc 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 decederadadedecedecererarea 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression and secretion vectors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This is the one of a pair of primers (see also AAX59389) used in the PCR amplification of a portion of the Saccharomyces cerevisiae genome incorporating the newly identified D9798.4 essential gene (see AAX59382). The primers hybridise to a portion of the 5' and 3' sequences flanking the D9798.4 open reading frame and include nucleotides that are homologous to the HIS3 selectable marker. The PCR product was used to construct a yeast strain in which the D9798.4 gene was deleted in order to confirm that this gene is essential for yeast survival. The D9798.4 gene is a homologue of the Aspergillus nidulans AN97 gene (see AAX59378). The genes and their encoded polypeptides can be used to identify homologous genes in other organisms and to identify novel antifungal or
                                                                                                                                                                                                                                                                                                                                                                       Aspergillus nidulans nucleic acids encoding essential proteins AN97, AN80, AN85 and AN17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 62 BP; 13 A; 19 C; 12 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 20; 78pp; English
                                                                                                                                                    98WO-US023874.
                                                                                                                                                                                              97US-00965762
                                                                                                                                                                                                                                         (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 38.5
Matches 20; Conservative
                    Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                    Gavrias V;
                                                                                                                                                                                                                                                                                                                              WPI; 1999-418430/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anti-yeast agents
                                                                                                                                                 09-NOV-1998;
                                                                                                                                                                                              07-NOV-1997;
                                                              WO9924580-A2
                                                                                                         20-MAY-1999
                                                                                                                                                                                                                                                                                    Koltin Y,
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Search completed: June 19, 2007, 14:04:59
                                     Job time : 317 secs
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23.3%; Score 18.4; DB 2; Length 62; 38.5%; Pred. No. 1.5e+04; Live 11; Mismatches 21; Indels

Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.

Homo sapiens EP1033401-A2

Dumas Milne Edwards J, Duclert A, Giordano J;

(GEST) GENSET.

26-FEB-1999;

21-FEB-2000; 2000EP-00200610

06-SEP-2000

Human secreted protein 5' EST, SEQ ID NO: 15806.

(first entry)

06-OCT-2000

AAC11731;

AAC11731 standard; cDNA; 65 BP

RESULT 15

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Gaps

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6; Indels

Score 18.4; DB 3; Pred. No. 1.5e+04; 2; Mismatches 6;

23.3%;

Length 65;

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DNA (genomic)
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US-08-014-723-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-014-723-12/c
                                                                                                                                                                                                                              June 19, 2007, 14:28:35 ; Search time 129 Seconds (without alignments) 1145.873 Million cell updates/sec
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Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Section | Compared |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12,
Sequence 12,
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Sequence
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GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd.
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US-09-513-999C-14603
US-08-014-723-11
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US-08-965-762-27
US-09-911-927-27
US-09-911-882-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -09-475-947A-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1403666 seqs, 935554401 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                      - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDENTITY NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                 US-10-604-726A-5135
79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq length: 0 seq length: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query
                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB 8
Maximum DB 8
                                                                                                                                                      OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Result
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Appl	Appl	Appl	Appl	-	App	Appl	Appl	Appl	Appl	Appl	Appl	Appl	48, A	240, App	Appli	Appli	App.	App		Appl	Appl	
16,	16,	16,	25,	847	847	53,	53,	23,	13,	13,	13,	13,	13448,	240	7,	7	137	137,	1570	12,	14,	
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	
US-08-475-610-16	PCT-US92-00277-16	PCT-US92-00278-16	US-09-844-508-25	US-10-131-827-847	US-10-131-831-847	US-08-790-963-53	US-09-371-774-53	US-09-875-082-53	US-08-433-126A-13	US-08-433-124A-13	US-08-976-413A-13	PCT-US96-06059-13	US-09-621-976-13448	US-09-804-980-240	US-09-564-805-7	US-09-434-382-7	US-09-275-850-137	US-09-907-111-137	US-09-513-999C-15701	US-09-281-481A-12	US-09-281-481A-14	
m	7	7	Ŋ	ო	വ	~	m	ო	~	~	m	7	m	4	m	m	m	m	m	m	m	
78	78	78	77	20	20	29	29	29	72	72	72	72	24	9	65	65	72	72	78	43	43	
22.8	22.8	22.8	22.5	22.3	22.3	22.3	22.3	22.3	22.0	22.0	22.0	22.0	21.8	21.8	21.8	21.8	21.8	21.8	21.8	21.5.	21.5	
18	18	18	17.8	17.6	17.6	17.6	17.6	17.6	17.4	17.4	17.4	17.4	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17	17	
24	22	56	27	28	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45	
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TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: D.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
ZITY: Arlington
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                  Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 65;
                                                                                                                                                                                                                                                                                                                                                                                1 GGAGGGCGGGGGAGACGAGCGGCUCUGGCCCCUUAAUU 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                   47 egecedecedecececacadedecececececece
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 19; DB 2;
Pred. No. 1.1e+03;
3; Mismatches 10
                                                                                                                                                                                                                                                                                                    24.3%; Score 19.2; DB 3; 60.0%; Pred. No. 8.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       For Preparing the Same
18
                              Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/014,723
FILING DATE: 19930208
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Oblon, No. 5273962man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/08014723
Patent No. 5273962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Doi, Takeshi
APPLICANT: Iwasaki, Akio
APPLICANT: Iwasaki, Akio
APPLICANT: Kimura, Shigeru
APPLICANT: Ohkuchi, Masao
TITLE OF INVENTION: Thrombin-
TITLE OF INVENTION: Thrombin-
TITLE OF INVENTION: FOR PEPER NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.1%;
62.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (703)413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 65 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 62.9
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 60.0
Matches 24; Conservative
                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                      US-09-513-999C-14603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-014-723-11
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                                                                                                                                                                                                                                                                                                                                                                                                  Thrombin-Binding Substance and Process
For Preparing the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: Arlington
                          Length 63;
                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/110,011A
FILING DATE: 23-AUG-1993
CLASSIFICATION: 415
ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 AGGGCGGGGGAGAGACGAGCGGCUCUGGCCCCUUAAUUG 41
                                                                                                                                         40 AGGICGACGACGAGGCCAGCGGCTCTGGCGACTGACTCG 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 Aggacagagagagacaacaacaacacucuaaccccuuaauug
                      Score 19.8; DB 2;
Pred. No. 5.6e+02;
4; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 80-073-0 DIV TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14603, Application US/09513999C Patent No. 6783961
GENERAL INFORMATION: APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Ducalert, A. APPLICANT: Giordano, J.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DESCRIPTION: Other nucleic acid;
                                                                                                                                                                                                                                               Application US/08110011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5354664man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.1%;
59.0%;
                            25.1%;
59.0%;
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                                                                                                                                                                                                                                                                                                                                                                      Kimura, Shigeru
Ohkuchi, Masao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                        Doi, Takeshi
Iwasaki, Akio
Saino, Yushi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 25.1
Best Local Similarity 59.0
Matches 23; Conservative
                              Query Match
Best Local Similarity 59.0°
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Th
TITLE OF INVENTION: FOI
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 63 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                      Patent No. 5354664
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APPLICANT:
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44.7%; Pred. No. 1.2e+03;
tive: 9; Mismatches 12; Indels
a Modified Protease Cleavage Site
                                    STREET: Two Embarcadero Center, Eighth Floor STATE: CA Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 753, Application US/08444818
Fatent No. 6150087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NANBV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chirch C.
                                                                                                                                                                                                                          COMPUTER: IBM Compatible COMPUTER: IBM COMPATIONS
OPERATING SYSTEM: DOS
SOFTWARE: FastSEN for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/367,791A
FILING DATE: 12-No. 6573071-1999
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 CCAGAATCGATTCTCGTGTTGTTGTCGCCCCTCTC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 CCUUAAUUGUACUUCGGCUCGUAUUGUCUCUCCUTUC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 42,471
REFERENCE/DOCKET NUMBER: 20695D-000700US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: AT A 335/97
FILING DATE: 27-FEB-1997
APPLICATION NUMBER: WO PCT/AT98/00045
FILING DATE: 27-FEB-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-367-791A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/444,818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Ausenhus, Scott L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 576-0300
                                                                                                                                          COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 44.7%
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-444-818-753/c
                   NUMBER OF
                                                                                                                                                                                                                                                                                       Kimura, Shigeru
Ohkuchi, Masao
NVENTION: Thrombin-Binding Substance and Process
NVENTION: For Preparing the Same
                                                                                                                                                                                                                                                                                                                                                                                                                  OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
STRY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/08/110, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/110,011A
FILING DATE: 23-AUG-1993
TYORNEY APPLICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dorner, Friedrich
Fisch, Andreas
Eibl, Johann
TITLE OF INVENTION: Factor X Analogues With
                                                        30 AGGTCGACGACGAGCCAGCGGCTCTGGCGACTGA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.1%; Score 19; DB 2; 1 62.9%; Pred. No. 1.1e+03; Live 3; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 AGGGCGGGGAGAGACGAGCGGCUCUGGCCCCUUA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 Aggregacgaegaegecagegereregegaerea 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: Other nucleic acid; DESCRIPTION: DNA (synthetic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Himmelspach, Michele
                                                                                                                                                           Sequence 11, Application US/08110011A
Patent No. 5354664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19, Application US/09367791A Patent No. 6573071 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5354664man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schlokat, Uwe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (703)413 - 3000
                                                                                                                                                                                                                        Doi, Takeshi
Iwasaki, Akio
Saino, Yushi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (703)413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 62.9
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS ADDRESSEE: OBLON, SI
                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Doi, Ta
APPLICANT: Iwasaki
APPLICANT: Saino,
APPLICANT: Kimura,
APPLICANT: Ohkuchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 bases
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ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                       RESULT 5
US-08-110-011A-11
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US-09-367-791A-19
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                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 18.8; DB 3; Length 79;
; Pred. No. 1.4e+03;
11; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 27, Application US/08965762;
Sequence 27, Application US/08965762;
Patent No. 6280963;
GENERAL INFORMATION:
APPLICANIT: KOLILI, Yigal
TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE
FILE REFERENCE: 07334/06201;
CURRENT APPLICATION NUMBER: US/08/965,762
CURRENT FILING DATE: 1997-11-07;
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FREESEQ for Windows Version 3.0
; SEQ ID NO 27
LENGTH: 62
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TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE
FILE REPERENCE: 62286-0622003
CURRENT APPLICATION NUMBER: US/09/911,927
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 08/965,762
PRIOR FILING DATE: 1997-11-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.3%; Score 18.4; DB 3;
38.5%; Pred. No. 1.9e+03;
tive 11; Mismatches 21;
                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REGISTRATION NUMBER: NEXOT/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27, Application US/09911927
Patent No. 6461826
GENERAL INFORMATION:
APPLICANT: Koltin, Yigal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                 23.8%;
38.7%;
10-JUNE-1991
                                                              FILING DATE: 11-JUNE-1990
                                                                                                                                                                                                              TELLEPAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 41.
SEQUENCE CHARACTERISTICS:
LENGTH: 79 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 38.7%
Matches 24; Conservative
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Matches 20; Conserv
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    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                  ;
TOPOLOGY:
US-08-687-421-415
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US-09-911-927-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF BASIC TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR AND TITLE OF INVENTION: THROWBIN CORRESPONDENCES: 445
CORRESPONDENCES: 8445
ADDRESSES: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diskette, 3.5 inch, 1.44 MB storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 23.8%; Score 18.8; DB 3; Best Local Similarity 48.1%; Pred. No. 1.3e+03; Matches 26; Conservative 6; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                            /desc = "primer JHC 13"
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APPLICATION NUMBER: US/08/687,421
FILING DATE: 08-MAY-1996
                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
                                                                            US/08/403,590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 415, Application US/08687421 Patent No. 6177557 GENERAL INFORMATION:
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FILING DATE: 11.NOVEMBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
                                                                                                                                                                                                                                                                                                                                                                                                      other nucleic acid
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/195,005
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 22-APRIL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/219
FILING DATE: 28-MARCH-1994
PRIOR APPLICATION DATA:
                                                                                                                                        NAME: Harbin, Alisa A. REGISTRATION NUMBER: 33,895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 6.0
                                                                                                                                                                                                                           TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 753
SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gold, Larry
APPLICANT: Janjic, Nebojsa
APPLICANT: Tasset, Diane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS
                                                                                           FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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US-08-687-421-415
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SEQ ID NO 15806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 65
                       Query Match
Best Local (
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                                                                 Matches
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                                                                                                                                                                                                                                                                                                 27 CUGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUCUCCUUUCGCCACCUC
                                                                                                                                                                                                                Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.3%; Score 18.4; DB 3; Length 62; 38.5%; Pred. No. 1.9e+03;
                                                                                                                                                                                                                                                       21; Indels
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Patent No. 6514715
GENERAL INFORMATION:
TITLE OF INVENTION SESENTIAL FUNGAL GENES AND THEIR USE
TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE
CURRENT APPLICATION NUMBER: US/09/911,888
CURRENT APPLICATION NUMBER: US/09/911,888
PRIOR APPLICATION NUMBER: US/09/911,888
PRIOR FILING DATE: 1997-11-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Koltin, Yigal
APPLICANT: Koltin, Yigal
APPLICANT: Gavrias, Victoria
TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR ITLE REPERENCE: 06286-062004
CURRENT APPLICATION NUMBER: US/09/911,882
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 08/965,762
PRIOR PILING DATE: 1997-11-07
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                            Query Match 23.3%; Score 18.4; DB 3; Best Local Similarity 38.5%; Pred. No. 1.9e+03; Matches 20; Conservative 11; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Mismatches
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
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SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 27
LENGTH: 62
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                                                                                                                                    ; OTHER INFORMATION: primer for PCR US-09-911-927-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: primer for PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: primer for PCR US-09-911-888-27
                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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US-09-911-888-27
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LENGTH: 62
                                       SEQ ID NO 27
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Matches
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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.052.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
RIOR PELLING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
                                                                                                   Gaps
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         Length 62;
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                                                                                               Indels
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STREET: WASANDRIA
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/086,410
; Score 18.4; DB 3;
; Pred. No. 1.9e+03;
11; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l; DB 3;
1.9e+03;
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APPLICANT: LOISON, Gerard
APPLICANT: PESSEGUE, Bernard
APPLICANT: SHIRE, David
TITLE OF INVENTION: Artificial promoter for
TITLE OF INVENTION: of proteins in yeast
CORRESPONDENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.96
2; Mismatches
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Pred. No. 1.
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; Sequence 15806, Application US/09513999C
; Patent No. 6783961
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CLASSIFICATION: 435
FRICA APPLICATION DATA:
APPLICATION NUMBER: US 07/768,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 28, Application US/08086410; Patent No. 5407822; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
         23.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.3%;
71.4%;
                                                                                                   20; Conservative
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Best Local Similarity 71.4
Matches 20; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                    Similarity
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Gaps
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APPLICANT: Wren, Jonathan D.
APPLICANT: Wren, Jonathan D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
FILE REFERENCE: UTSD0667
CURRENT APPLICATION NUMBER: US/09/475,947A
CURRENT FILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 23.0%; Score 18.2; DB 2; Best Local Similarity 58.1%; Pred. No. 2.3e+03; Matches 18; Conservative 5; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18; DB 3; Pred. No. 2.4e+03; 2; Mismatches 10
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FILING DATE: 02-OCT-1991
APPLICATION NUMBER: FR 89 17467
FILING DATE: 29-DEC-1989
ATTORNEY AGENT INFORMATION:
NAME: SAXE, BETTLAND B.
REGISTRATION NUMBER: 28,665
REGISTRATION NUMBER: 16781/318
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 683-9300
TELEFAX: (703) 683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
IMMEDIATE SOURCE:
CLONE: Hind III - ECORI fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-475-947A-86/c
; Sequence 86, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 GGAGAGACGAGCGGCUCUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 899149
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 65 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 22.8
Best Local Similarity 64.7
Matches 22; Conservative
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CRGANISM: human
US-09-475-947A-86
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Search completed: June 19, 2007, 15:45:42 Job time : 131 secs

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1: FBMC Celerra_SIDS3/ptcdata/2/pubpna/USO7_PUBCOMB. Beq:*
2: FBMC Celerra_SIDS3/ptcdata/2/pubpna/USO8_PUBCOMB. Beq:*
3: FBMC Celerra_SIDS3/ptcdata/2/pubpna/USO8_PUBCOMB. seq:*
4: FBMC Celerra_SIDS3/ptcdata/2/pubpna/USO9_PUBCOMB. seq:*
5: FBMC Celerra_SIDS3/ptcdata/2/pubpna/USO9_PUBCOMB. seq:*
6: FBMC Celerra_SIDS3/ptcdata/2/pubpna/USO0_PUBCOMB. seq:*
7: FBMC Celerra_SIDS3/ptcdata/2/pubpna/USIOB_PUBCOMB. seq:*
8: FBMC Celerra_SIDS3/ptcdata/2/pubpna/USIOB_PUBCOMB. seq:*
10: FBMC Celerra_SIDS3/ptcdata/2/pubpna/USIOF_PUBCOMB. seq:*
11: FBMC Celerra_SIDS3/ptcdata/2/pubpna/USIOF_PUBCOMB. seq:*
12: FBMC Celerra_SIDS3/ptcdata/2/pubpna/USIOF_PUBCOMB. seq:*
13: FBMC Celerra_SIDS3/ptcdata/2/pubpna/USIOF_PUBCOMB. seq:*
14: FBMC Celerra_SIDS3/ptcdata/2/pubpna/USIOF_PUBCOMB. seq:*
15: FBMC Celerra_SIDS3/ptcdata/2/pubpna/USIOF_PUBCOMB. seq:*
16: FBMC Celerra_SIDS3/ptcdata/2/pubpna/USIOF_PUBCOMB. seq:*
17: FBMC Celerra_SIDS3/ptcdata/2/pubpna/USIOF_PUBCOMB. seq:*
18: FBMC Celerra_SIDS3/ptcdata/2/pubpna/USIOF_PUBCOMB. seq:*
18: FBMC Celerra_SIDS3/ptcdata/2/pubpna/USIOF_PUBCOMB. seq:*
19: FBMC Celerra_SIDS3/ptcdata/2/pubpna/USIOF_PUBCOMB. seq:*
10: FBMC Celerra_SIDS3/ptcdata/2/pubpna/USIOF_PUBCOMB. seq:*
11: FBMC Celerra_SIDS3/ptcdata/2/pubpna/USIOF_PUBCOMB. seq:*
12: FBMC Celerra_SIDS3/ptcdata/2/pubpna/USIOF_PUBCOMB. seq:*
13: FBMC Celerra_SIDS3/ptcdata/2/pubpna/USIOF_PUBCOMB. seq:*
14: FBMC Celerra_SIDS3/ptcdata/2/pubpna/USIOF_PUBCOMB. seq:*
15: FBMC Celerra_SIDS3/ptcdata/2/pubpna/USIOF_PUBCOMB. seq:*
16: FBMC Celerra_SIDS3/ptcdata/2/pubpna/USIOF_PUBCOMB. seq:*
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17: FBMC Celerra_SIDS3/ptcdata/2/pubpna/USIOF_PUBCOMB. seq:*
18: FBMC Celerra_SIDS3/ptcdata/2/pubca/2/pubca/2/pubca/2/pubca/2/pubca/2/pubca/2/pubca/2/pubca/2/pubca/2/pubca/2/pubca/2/pubca/2/pubca/2/pubca/2/pubca/2/pubca/2/pubca/2/pubca/2/pubca/2/pubca/2/pubca/2/pubca/2/pubca/2/pubca/2/pubca
                                                                                                                                                                                                                                                                                                                                          June 19, 2007, 14:41:36; Search time 744 Seconds (without alignments) 1304.735 Million cell updates/sec
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/EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
/EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
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GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18892170 seqs, 6143817638 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                      OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0 Maximum DB seq length: 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Su Que	TYPE: ORGANI 3-10-310- Query Ma Best Loc Matches	医200 万单	A Human 4A-1661 h Simila Simila	NA M: Human 14A-16611 34 ch. 34 1 Similarity 80 28; Conservative	34.2%; 80.0%; vative		Sco Pre 2;	Score 27; Pred. No.	re 27; DB d. No. 6.8; Mismatches	11,	Length 5; Indel	ngth 67 Indels	0 ,7		Gaps	.0			*
	£ & 8	a com	-	n	COMBETVALIVE 2; MISHIALCHES GAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GGAGA(sacg 	A /	ACCCC	acche 1960 1960 1960	m m	 		•		2 0 0	5			
•	RESULT US-10- Sequ Publ GEND APP HITT TIT	ULT 2 10-448 equency ublica PEREMA APPLICA APPLICA TITLE TITLE TITLE	SULT 2 -10.448-250-6 Sequence 6, Applicat Publication No. US20 GENERAL INFORMATION: APPLICANT: Mendons TITLE OF INVENTION: TITLE OF INVENTION: FILE REFERENCE: 110 CURRENT APPLICATION	D-6 APP N NO. FORMA: BOW INVENIENCEN	·4 0 2 10 ·	on US/10448250 140018530A1 1ichael T Shaun D ELECTROPHORETIC SI 01870101 NUMBER: US/10/448;	1044 30A1 T T C E 30 E 30 E	:8250 :VOLU :/10/	TIC 1C	N OF FUNC SELECTION	UNCTE	OF FUNCTIONAL RNA AND LECTION	NA A	AND DNA	AN US	USING			•	•

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Gaps
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APPLICANT: Hahn, Frederick
APPLICANT: Kuehnle, Adelheid
TITLE OF INVENTION: Manipulation of genes of the mevalonate and i
TITLE OF INVENTION: create novel traits in transgenic organisms
FILE REFERENCE: KAS-103XC1
CURRENT APPLICATION NUMBER: US/09/918,740
CURRENT FILING DATE: 2001-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , OTHER INFORMATION: Oligonucleotide containing S. cerevisiae DNA US-09-918-740-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 39;
                                                                                                                               COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATION SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/10/407,123
FILING DATE: 04-Apr-2003
CLASSIPICATION: <universely.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 CCUUAAUUGUACUUCGGGCUCGUAUUGUCUCUCCUUUC 70
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/367,791A
FILING DATE: 12-No. US20030181381A1-1999
APPLICATION NUMBER: AT A 335/97
FILING DATE: 27-FEB-1997
APPLICATION NUMBER: WO PCT/AT98/00045
FILING DATE: 27-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,471
REFERENCE/DOCKET NUMBER: 20695D-000700US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 18.8; DB 3;
Pred. No. 8.2e+03;
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Pred. No. 7.6e+03;
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MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/221,703
PRIOR FILING DATE: 2000-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15, Application US/09918740 Publication No. US20030033626A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION
                                                            ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 76
SOFWARE: Patentin version 3.0
SEQ ID NO 12
LENGTH: 72
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28.3%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 19:
San Francisco
                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17; Conservative
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Best Local Similarity
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Best Local Similarity
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APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 66087.020.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                6 GCGGGGGAGAGAGGAGCGGCUCUGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUCUC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAGCACAGAGGTCAGATGTTGTGTACCGTTATTTGTGCCTCAGCATCCCCGTGGCTAAC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 24;
                                                                                                                                                                                                                                                                                                                                                      Length 80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.8%; Score 18.8; DB 11; 90.9%; Pred. No. 7.1e+03;
                                                                                                                                                                                                                                                                                                                                                      Score 19.2; DB 8;
Pred. No. 5.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 37212, Application US/10310914A Publication No. US20060003322Al GENERAL INFORMATION:
                     PRIOR APPLICATION NUMBER: 60/384,709
PRIOR FLING DATE: 2002-05-31
PRIOR PRILING DATE: 2002-05-31
PRIOR FILING DATE: 2003-05-15
NUMBER OF SEQ ID NOS: 127
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6
LENGTH: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Himmelspach, Michele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGAGGGGGGGGAGAGACGAGC 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schlokat, Uwe
Dorner, Friedrich
Fisch, Andreas
                                                                                                                                                                                                                                                                                                                                                      24.3%;
                                                                                                                                                                                                                                     ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 35.9%
Matches 23; Conservative
                                                                                                                                                                                                                                                                                   OTHER INFORMATION: aptamer
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Best Local Similarity
Matches 20; Conserv
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ORGANISM: Human
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                                                                                                                                                                                                                  TYPE: DNA
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APPLICANT: WASSERMAN, Alon
APPLICANT: WINTZ, E1
APPLICANT: MINTZ, E1
APPLICANT: MINTZ, Liac
APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REFERENCE: 36689-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
                                                                                                                                                                                                                                                                                 APPLICANT: Masliah, Eliezer
APPLICANT: Masliah, Eliezer
APPLICANT: Masliah, Eliezer
APPLICANT: Hashimoto, Maktoo
APPLICANT: Rockenstein, Edward
TITLE OF INVENTION: METHODS FOR TESTING AND SELECTION OF INHIBITORS WITH
TITLE OF INVENTION: MEURODEGENERATIVE DISEASE
TITLE OF INVENTION: NEURODEGENERATIVE DISEASE
TITLE OF INVENTION: NEURODEGENERATIVE DISEASE
FILE REFERENCE: 6627-PA9013
CURRENT APPLICATION NUMBER: US/10/853, 774
CURRENT FILING DATE: 2004-05-24
PRIOR APPLICATION NUMBER: US/09/806,842
PRIOR APPLICATION NUMBER: DEC/09/806,842
PRIOR PILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: PCT/US99/23134
PRIOR FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 CGATGTFCCCTGCCCCTCCACTGTCTTCTGGGCTACTGCTGTCACACC 1
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72 CCTTAATTGTTCTTCATCATAATCCTTTTTCTCTTGTTGGGAACTC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19; Indels
                                                                                                                                                                                                                                                       APPLICANT: Regents of the University of California APPLICANT: Masliah, Eliezer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 23.5%; Score 18.6; DB 3; Best Local Similarity 63.6%; Pred. No. 9.6e+03; Matches 21; Conservative 3; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.4e+03;
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Pred. No. 9.4e+
9; Mismatches
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PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3993, Application US/09908975
Publication No. US20030165843A1
                                                                                                                                                                    Sequence 3, Application US/10853774 Publication No. US20050086711A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 42.99
Matches 21; Conservative
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SOFTWARE: Patentin version
SEQ ID NO 3993
LENGTH: 65
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Publication No. US20050241017A1

GENERAL INFORMATION:
APPLICANT: Hahn, Frederick
APPLICANT: Kuehnle, Adelheid
TITLE OF INVENTION: Manipulation of genes of the mevalonate and isoprenoid pathways tritle OF INVENTION: Application of genes of the mevalonate and isoprenoid pathways tritle OF INVENTION: Create novel traits in transgenic organisms
FILE REFERENCE: KAS-103XC1
CURRENT FPLIANG DATE: 2005-02-08
FRIOR APPLICATION NUMBER: US/11/053,541
FRIOR APPLICATION NUMBER: G0/221,703
FRIOR FILING DATE: 2001-07-31
FRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 76
SEQ ID NOS: 76
SEQ ID NO 15
LENGTH: 72
LENGTH: 72
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hahn, Frederick
APPLICANT: Kuehnle, Adelheid
TITLE OF INVENTION: Manipulation of genes of the mevalonate and isoprenoid pathways to TITLE OF INVENTION: Manipulation of genes of the mevalonate and isoprenoid pathways to TITLE OF INVENTION: create novel traits in transgenic organisms
FILE REFERENCE: KAS-103XC1
CURRENT APPLICATION NUMBER: US/10/835,516
CURRENT APPLICATION NUMBER: US/09/918,740
PRIOR FILING DATE: 2001-07-31
PRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.0
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  Gaps
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US-10-835-516-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 23.8%; Score 18.8; DB 9; Length 72; 1 Similarity 28.3%; Pred. No. 8.2e+03; 13; Conservative 16; Mismatches 17; Indels
                                                       33 CCUUNAUUGUACUUCGGGCUCGUAUUGUCUCCCUCUUUCGCCACCUC 78
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  Indels
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72 CCTTAATTGTTCTTCATCATAATCCTTTTTCTCTTGTTGGGAACTC
  17;
16; Mismatches
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; Sequence 15, Application US/10835516
; Publication No. US20040194162A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 28.34
Matches 13; Conservative
13; Conservative
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Best Local Similarity
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Matches
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33 CCUUAAUUGUACUUCGGGCUCGUAUUGUCUCUCCUUUCGCCACCUC 78

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US-11-175-859-73819
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| Sequence 47265, Application No. US2006002471541
| GENERAL INFORMATION:
| APPLICANT: Affymetrix, Inc. |
| APPLICANT: Affymetrix, Inc. |
| TILE OF INVENTION: Method of Analysis of Human Polymorphism FILE REFERENCE: 3690.11/175,859
| CURRENT APPLICATION NUMBER: US/11/175,859
| CURRENT APPLICATION NUMBER: US 60/585,352
| PRIOR PILING DATE: 2005-07-05
| PRIOR FILING DATE: 2004-07-02
| NUMBER OF SEQ ID NOS: 116251
| SEQ ID NO 47265
| LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.3%; Score 18.4; DB 16; Length 50; 41.3%; Pred. No. 1.1e+04;
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Pred. No. 9.9e+03;
8; Mismatches 24; Indels
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                                                                                            RESULT 10
US-10-384-245-10/c
; Sequence 10, Application US/10384245
; Publication No. US20040072191A1
; GENERAL INFORMATION:
; APPLICANT: Alex Chenchik
; TITLE OF INVENTION: Antisense RNA Standardizing Control; FILE REFERENCE: CLON-087PRV
; CURRENT APPLICATION NUMBER: US/10/384,245
; CURRENT PILING DATE: 2003-03-07
; NUMBER OF SEQ 1D NOS: 1090
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: GAVIAS, VICTORIA
TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE
FILE REPERENCE: 06206-06200C
CURRENT APPLICATION NUMBER: US/09/911,888
CURRENT FILING DATE: 2001-07-23
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                         40 AGCCTGAGGACAGAGGAGTGGCTCTGCCCCAT
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US-11-175-859-47265
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Best Local Similarity
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Matches 25; Conserv
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LENGTH: 80
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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; Sequence 73819, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT FILING DATE: 2005-07-05
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: Patentin Version 3.2
; SEQ ID NO 73819
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APPLICANT: Gavias, Victoria
TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE
TITLE REFERENCE: 06286-062003
CURRENT APPLICATION NUMBER: US/09/911,927
CURRENT APPLICATION NUMBER: US/09/911,927
PRIOR APPLICATION NUMBER: US/09/911,027
PRIOR FILING DATE: 2001-07-23
PRIOR FILING DATE: 2007-11-07
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 27
                                                                                                                                                                                                                                                                                            Query Match 23.3%; Score 18.4; DB 3; Best Local Similarity 38.5%; Pred. No. 1.1e+04; Matches 20; Conservative 11; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.3%; Score 18.4; DB 3; 38.5%; Pred. No. 1.1e+04;
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PRIOR APPLICATION NUMBER: US 08/965,762
PRIOR FILING DATE: 1997-11-07
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 27
LENGTH: 62
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Publication No. US20020142363A1
GENERAL INFORMATION:
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                                                                                                                                                                                                      FEATURE:

OTHER INFORMATION: primer for PCR US-09-911-888-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: homo sapien
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Best Local Similarity
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Sequence 10452, Application US/09908975

Publication No. US20030165843A1

GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi

APPLICANT: WASSERMAN, Alon
APPLICANT: WINTZ, Eli
APPLICANT: MINTZ, Eli
APPLICANT: MINTZ, Eli
APPLICANT: MINTZ, LIBERAN, AND SPLICE
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908, 975
CURRENT APPLICATION NUMBER: US/09/908, 975
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  23.0%; Score 18.2; DB 16; Length 50; 35.9%; Pred. No. 1.3e+04; tive 12; Mismatches 13; Indels (
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                                                                                                  41 GUACUUCGGCUCGUAUUGUCUCCUUUCGCCACCUCC 79
                                                                                                                              39 GTCCTTCTTCTTCMTATCGTTCATCCTTTTCCCACCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||::| ::|:|| 53 CCTTAGTTGTACATGTTGCACGTAATGGCTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR PLING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: Patentin version 3.0
EMORTH: 60
Query Match
Best Local Similarity 35.94
Matches 14; Conservative
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CORGANISM: Homo sapiens
US-09-908-975-10452
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US-09-908-975-10452/c
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Search completed: June 19, 2007, 15:35:39 Job time : 745 secs

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Sequence Sequence Sequence Sequence Sequence Sequence

Sequence

Sequence

39117, 145738,

295048

189867,

Sequence Sequence

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Scoring table:

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Sequence

439301, 546370,

626880

Sequence Sequence Sequence

276984,

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Sequence

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Sequence Sequence

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DB 11; Length 32;
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; Publication No. US20060257851A1
; GENERAL INPORMATION:
JAPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF PTILLE OF INVENTION: GENES AND USES THEREOF
; TITLE OF INVENTION: BOOT 0300. PCUS13;
CURRENT APPLICATION NUMBER: US/10/536,560
; CURRENT FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 424571
; SOFTWARE: Patentin Version 3.3
; SEQ ID NO 26233
                              US-11-130-645A-66022

US-11-130-645A-90177

US-11-130-645A-51247

US-11-130-645A-51249

US-11-130-645A-51349

US-11-130-645A-89154

US-11-130-645A-89154

US-11-130-645A-39177

US-11-130-645A-39177

US-11-130-645A-39179

US-11-130-645A-39179

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US-11-130-645A-39179

US-11-130-645A-39179

US-11-130-645A-39179

US-11-130-645A-3920

US-11-130-645A-10292

US-11-130-645A-10292

US-11-130-645A-395089

US-11-130-645A-10292

US-11-130-645A-10292
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Publication No. US20070050146A1
GENERAL INFORMATION:
APPLICANT: BENTWICH, Itzhak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
 ; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-536-560-26233
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Matches 21; Conserv
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2: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
3: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
4: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
5: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
6: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
7: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
8: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
9: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
11: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
12: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
13: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
14: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
15: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
16: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
17: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
18: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
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Sequence 109784,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22287, A
Sequence 169416,
Sequence 348741,
Sequence 498699,
Sequence 245318,
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156960,
243478,
385098,
                                                                                                                June 19, 2007, 15:23:21; Search time 2967 Seconds (without alignments) 274.926 Million cell updates/sec
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Sequence
Sequence
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                GenCore version 6.2.1 (c) 1993 - 2007 Biocceleration Ltd.
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US-11-130-645A-109784
US-11-130-645A-169416
US-11-130-645A-189411
US-11-130-645A-498699
US-11-130-645A-45318
US-11-130-645A-15960
US-11-130-645A-15960
US-11-130-645A-15960
US-11-130-645A-1598
                                                                                                                                                                                                                                                                                                                15754707 segs, 5162687648 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                   nucleic search, using sw model
                                                                                                                                                                                                                                                            IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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79
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                              Copyright
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Match
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227.3
27.3
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UNKARNI FILLING DATE: 2005-05-14
PRIOR APPLICATION NUMBER: PCT/USO5/16986
PRIOR PILING DATE: 2005-05-14
PRIOR PLLING DATE: 2005-05-14
PRIOR FILING DATE: 2004-05-14
PRIOR PLICATION NUMBER: US 10/709,572
PRIOR PLICATION NUMBER: US 60/666,340
PRIOR PLIING DATE: 2005-03-30
PRIOR PLLING DATE: 2005-03-25
PRIOR PLLING DATE: 2005-03-25
PRIOR PLLING DATE: 2005-03-17
PRIOR PLLING DATE: 2005-03-17
PRIOR PLLING DATE: 2005-03-17
PRIOR PLLING DATE: 2005-03-25
PRIOR PLLING DATE: 2005-03-17
PRIOR PLLING DATE: 2005-03-17
PRIOR PLLING DATE: 2005-03-17
PRIOR PLLING DATE: 2005-01-06
PRIOR PLLING DATE: 2004-11-16
PRIOR PLLING DATE: 2004-11-15
PRIOR PLLING DATE: 2004-11-15
PRIOR PLLING DATE: 2004-11-15
PRIOR PLLING DATE: 2004-11-15
PRIOR PLLING DATE: 2004-11-16
PRIOR PLING DATE: 2004-11-16
PRIOR PLING DATE: 2004-11-16
PRIOR APPLICATION NUMBER: US 60/522,860
PRIOR FILING DATE: 2004-11-15
PRIOR PILING DATE: 2004-11-15
PRIOR PILING DATE: 2004-0-04
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 76616
SOFTWARE: Patentin version 3.3
SEQ ID NO 22287
LENGTH: 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 64;
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APPLICANT: Amir, Avniel
APPLICANT: Yael, Karov
APPLICANT: Yael, Karov
APPLICANT: Ranit, Aharonov
ITITLE OF INVENTION: Micrornas and Uses Thereof
FILE REFERENCE: 06087.0202.CPUS13
CURRENT APPLICATION NUMBER: US/11/130,645A
CURRENT FILING DATE: 2005-05-16
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Best Local Similarity 37.8
Matches 17; Conservative
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Best Local Similarity 37.8
Matches 17; Conservative
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; ORGANISM: Homo sapiens
US-11-130-645A-169416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
US-11-130-645A-22287
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30.6%; Score 24.2; DB 19; Length
Best Local Similarity 37.8%; Pred. No. 3.3e+02;
Matches 17; Conservative 15; Mismatches 13; Indels
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APPLICANT: Amir, Avniel
APPLICANT: Yael, Karov
APPLICANT: Anait, Abaronov
TITLE OF INVENTION: Micrornas and Uses Thereof
FILE REFERENCE: 06087.0202.CPUS13
CURRENT APPLICATION NUMBER: US/11/130,645A
                                                                                                                                                                                                  HITLE OF INVENTION: Micrornas and Uses Thereof
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PRIOR PELICATION NUMBER: PCT/USOS/16986

PRIOR FILING DATE: 2005-05-14

PRIOR APPLICATION NUMBER: US 10/709,577

PRIOR APPLICATION NUMBER: US 10/709,572

PRIOR PILING DATE: 2004-05-14

PRIOR PILING DATE: 2005-03-30

PRIOR PILING DATE: 2005-03-30

PRIOR PILING DATE: 2005-03-25

PRIOR PAPLICATION NUMBER: US 60/665,094

PRIOR PILING DATE: 2005-03-25

PRIOR PELING DATE: 2005-03-17
                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2003-09-10
PRIOR PELING DATE: 2005-05-14
PRIOR PELING DATE: 2005-05-14
PRIOR APPLICATION NUMBER: PCT/109,577
PRIOR FILING DATE: 2004-05-14
PRIOR FILING DATE: 2004-05-14
PRIOR PLING DATE: 2004-05-14
PRIOR PILING DATE: 2004-05-14
PRIOR FILING DATE: 2005-03-30
PRIOR PELING DATE: 2005-03-30
PRIOR PELING DATE: 2005-03-30
PRIOR PELING DATE: 2005-03-32
PRIOR PELING DATE: 2005-03-17
PRIOR APPLICATION NUMBER: US 60/593,329
PRIOR PELING DATE: 2005-03-17
PRIOR PLING DATE: 2005-01-06
PRIOR PLING DATE: 2004-12-08
PRIOR PLING DATE: 2004-11-15
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CURRENT APPLICATION NUMBER: US/11/130,645A
CURRENT FILING DATE: 2005-05-16
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RAPLICATION NUMBER: US 60/665,094

RAPLICATION NUMBER: US 60/662,742

RILING DATE: 2005-03-17

RILING DATE: 2005-03-17

OR APPLICATION NUMBER: US 60/593,329

RAPLICATION NUMBER: US 60/593,081

RILING DATE: 2005-01-06

OR FILING DATE: 2004-12-08

OR PELING DATE: 2004-11-15

OR FILING DATE: 2004-11-15

OR PILING DATE: 2004-11-15
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PRIOR FILING DATE: 2005-01-06
PRIOR APPLICATION NUMBER: US 60/593,081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : PatentIn version 3.3
                                                                                                                                                             Ranit, Aharonov
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US-11-130-645A-109784
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US-11-130-645A-22287/c
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8

Gaps

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2 GAGGGCGGGGGAGAGACGAGCGCCUCUGGCCCCCUUAAUUGUACUUCGGGCCUCGUAU 57
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                          PRIOR APPLICATION NUMBER: US 60/662,742
PRIOR APPLICATION NUMBER: US 60/593,329
PRIOR FILING DATE: 2005-01-06
PRIOR FILING DATE: 2004-10-08
PRIOR FILING DATE: 2004-12-08
PRIOR FILING DATE: 2004-11-08
PRIOR FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: US 60/522,860
PRIOR FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: US 60/522,457
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PRIOR FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: US 60/522,457
PRIOR PILING DATE: 2004-10-04
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 760616
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APPLICANT: Yael, Karov
APPLICANT: Ranit, Aharonov
TITLE OF INVENTION: Micrornas and Uses Thereof
FILE REFERENCE: 06087.0202.CPUS13
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1-11-130-645A-245318/c
Sequence 245318, Application US/11130645A
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PRIOR FILING DATE: 2005-05-14
PRIOR PLING DATE: 2004-05-14
PRIOR FILING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: US 10/709,572
PRIOR PILING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: US 60/666,340
IG DATE: 2005-03-25
CATION NUMBER: US 60/662,742
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PRIOR APPLICATION NUMBER: US 60/665,094
PRIOR FILING DATE: 2005-03-25
PRIOR APPLICATION NUMBER: US 60/662,742
PRIOR FILING DATE: 2005-03-17
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PRIOR PILING DATE: 2005-01-06
PRIOR APPLICATION NUMBER: US 60/593,081
PRIOR FILING DATE: 2004-12-08
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SEQ ID NO 498699
LENGTH: 63
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US-11-130-645A-498699
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TITLE OF INVENTION: Micrornas and Uses Thereof
FILE REPERENCE: 06087.020.CPUS13
CURRENT APPLICATION NUMBER: US/11/130,645A
CURRENT PILING DATE: 2005-05-16
PRIOR APPLICATION NUMBER: US 10/709,577
PRIOR FILING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: US 10/709,577
PRIOR FILING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: US 60/66,340
PRIOR FILING DATE: 2005-03-10
PRIOR PELING DATE: 2005-03-10
PRIOR PELING DATE: 2005-03-17
PRIOR PELING DATE: 2005-03-17
PRIOR APPLICATION NUMBER: US 60/65,094
PRIOR PLING DATE: 2005-03-17
PRIOR PELING DATE: 2005-03-17
PRIOR PELING DATE: 2005-03-17
PRIOR PELING DATE: 2005-03-17
PRIOR PELING DATE: 2004-10-06
PRIOR FILING DATE: 2004-11-08
PRIOR FILING DATE: 2004-11-15
PRIOR FILING DATE: 2004-11-15
PRIOR FILING DATE: 2004-11-15
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PRIOR FILING DATE: 2004-11-15
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Publication No. US20070050146A1
GENERAL INFORMATION:
APPLICANT: Bentwin's Litzhak
APPLICANT: Amir, Avniel
APPLICANT: Amir, Avniel
APPLICANT: Ranit, Aharonov
ITILE REFERENCE: 06087.0202.CPUS13
FILE REFERENCE: 06087.0202.CPUS13
FILE REFERENCE: 06087.0202.CPUS13
FILE REFERENCE: 05087.0202.CPUS13
FRIOR APPLICATION NUMBER: US 10/709,577
FRIOR APPLICATION NUMBER: US 10/709,572
FRIOR PILING DATE: 2004-05-14
FRIOR PILING DATE: 2004-05-14
FRIOR PILING DATE: 2004-05-14
FRIOR PILING DATE: 2005-03-30
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                          US-11-130-645A-348741/c
; Sequence 348741, Application US/11130645A
; Publication No. US20070050146A1
; GENERAL INFORMATION:
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SEQ ID NO 348741
LENGTH: 64
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Best Local Similarity 37.8
Matches 17; Conservative
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US-11-130-645A-348741
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US-11-130-645A-498699/c
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TYPE: RNA
CORGANISM: Homo sapiens
US-11-130-645A-156960
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                                                      Indels
Best Local Similarity 48.2%; Pred. No. 1.3e+03;
Matches 27; Conservative 8; Mismatches 21;
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TITLE OF INVENTION: Micrornas and Uses Thereof
FILE REFERENCE: 06087.0202.CPUS13
CURRENT APPLICATION NUMBER: US/11/130,645A
CURRENT FILING DATE: 2005-05-16
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R PLING DATE: 2004-05-14

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R APPLICATION NUMBER: US 60/666,340

R APPLICATION NUMBER: US 60/666,340

R APPLICATION NUMBER: US 60/665,094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 651361, Application US/11130645A Publication No. US20070050146A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT/US05/16986
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FILING DATE: 2005-01-06
APPLICATION NUMBER: US 60/593,081
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APPLICANT: Bentwich, Itzhak
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Best Local Similarity 45.3*
Matches 29; Conservative
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; ORGANISM: Homo sapiens
US-11-130-645A-651361
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US-11-130-645A-156960
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 760616
SOFTWARE: PatentIn version 3.3
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Pred. No. 2.5e+03;
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APPLICANT: Amir, Avniel
APPLICANT: Yael, Karov
APPLICANT: Ranit, Aharonov
APPLICANT: Ranit, Aharonov
APPLICANT: Ranit, Aharonov
APPLICANT: Ranit, Aharonov
TITLE OF INVENTION: Micrornas and Uses Thereof
FILE REPERENCE: 06097.0202.CPUS13
CURRENT APPLICATION NUMBER: US 11/130,645A
CURRENT FILING DATE: 2005-05-16
PRIOR FILING DATE: 2005-05-14
PRIOR APPLICATION NUMBER: US 10/709,577
PRIOR APPLICATION NUMBER: US 60/66,340
PRIOR FILING DATE: 2004-05-14
PRIOR FILING DATE: 2005-03-30
PRIOR APPLICATION NUMBER: US 60/665,094
PRIOR FILING DATE: 2005-03-17
PRIOR FILING DATE: 2005-03-17
PRIOR FILING DATE: 2005-03-17
PRIOR FILING DATE: 2005-03-17
PRIOR APPLICATION NUMBER: US 60/593,329
PRIOR FILING DATE: 2005-03-17
PRIOR APPLICATION NUMBER: US 60/593,081
PRIOR PILING DATE: 2005-01-06
PRIOR PILING DATE: 2005-11-08
PRIOR PILING DATE: 2005-11-08
PRIOR PILING DATE: 2005-11-08
PRIOR FILING DATE: 2005-11-08
PRIOR FILING DATE: 2005-11-08
PRIOR FILING DATE: 2004-11-15
PRIOR PILING DATE: 2004-11-15
PRIOR PRILING DATE: 2004-11-15
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0; Mismatches
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CURRENT FILING DATE: 2005-05-16
PRIOR APPLICATION NUMBER: PCT/US05/16986
                                                                                                                  PRIOR PILING DATE: 2004-05-14
PRIOR PILING DATE: 2004-05-14
PRIOR PLING DATE: 2004-05-14
PRIOR PLING DATE: 2005-03-30
PRIOR PLING DATE: 2005-03-30
PRIOR PLING DATE: 2005-03-30
PRIOR PLING DATE: 2005-03-30
                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2005-03-25
PRIOR APPLICATION NUMBER: US 60/662,742
PRIOR PILING DATE: 2005-03-17
PRIOR APPLICATION NUMBER: US 60/593,329
PRIOR FILING DATE: 2005-01-06
PRIOR APPLICATION NUMBER: US 60/593,081
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                                                                                          PRIOR APPLICATION NUMBER: US 10/709,577
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Best Local Similarity 75.0%;
Matches 27; Conservative
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PRIOR APPLICATION UNBER: US 60/666,340

PRIOR FILING DATE: 2005-03-30

PRIOR PILING DATE: 2005-03-30

PRIOR PILING DATE: 2005-03-25

PRIOR PILING DATE: 2005-03-25

PRIOR PILING DATE: 2005-03-17

PRIOR PILING DATE: 2005-03-17

PRIOR PILING DATE: 2005-03-16

PRIOR PILING DATE: 2005-03-06

PRIOR PILING DATE: 2005-03-06

PRIOR PILING DATE: 2006-12-06

PRIOR PILING DATE: 2004-11-15

PRIOR PILING DATE: 2004-11-15

PRIOR PILING DATE: 2004-11-15

PRIOR PILING DATE: 2004-11-15

PRIOR PILING DATE: 2004-11-04

PRIOR APPLICATION NUMBER: US 60/522,457

PRIOR APPLICATION ADDATE: 2004-11-04

PRIOR PILING DATE: 2004-11-04

PRIOR PILING DATE: 2004-11-04

NUMBER OF SEQ ID NOS: 760616
                                                                                                                                            APPLICANT: Ranit, Aharonov
TITLE OF INVENTION: Micrornas and Uses Thereof
FILE REPERENCE: 0609.70202.CPUS13
CURRENT APPLICATION NUMBER: US/11/130,645A
CURRENT FILING DATE: 2005-05-16
                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT/USOS/16986
PRIOR PILING DATE: 2005-05-14
PRIOR APPLICATION NUMBER: US 10/709,577
PRIOR FILING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: US 10/709,572
PRIOR FILING DATE: 2004-05-14
                                                                                         Amir, Avniel
Yael, Karov
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Pred. No. 2.5e+03;
0; Mismatches 9;
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APPLICANT: Yael, Karov
APPLICANT: Yael, Karov
APPLICANT: Ranit, Aharonnov
TILE OF INVENTION: Micrornas and Uses Thereof
FILE REFERENCE: 06087.0202.CPUS13
CURRENT APPLICATION NUMBER: US/11/130,645A
PRIOR APPLICATION NUMBER: PCT/USOS/16986
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PRIOR APPLICATION NUMBER: US 10/709, 577
PRIOR PELING DATE: 2004-05-14
PRIOR PELING DATE: 2004-05-14
PRIOR PLING DATE: 2004-05-14
PRIOR PLING DATE: 2005-03-30
PRIOR APPLICATION NUMBER: US 60/665, 094
PRIOR APPLICATION NUMBER: US 60/662, 742
PRIOR APPLICATION NUMBER: US 60/62, 742
PRIOR APPLICATION NUMBER: US 60/62, 742
PRIOR APPLICATION NUMBER: US 60/593, 329
PRIOR APPLICATION NUMBER: US 60/593, 081
PRIOR PLING DATE: 2005-03-16
PRIOR PLING DATE: 2006-01-06
PRIOR PLING DATE: 2004-12-08
PRIOR PLING DATE: 2004-11-15
PRIOR PELING DATE: 2004-11-15
                 Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 760616
SOFTWARE: PatentIn version 3.3
SEQ ID NO 243478
LENGTH: 64
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Best Local Similarity 75.0%;
Matches 27; Conservative
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PRIOR FILING DATE: 2004-10-04
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Best Local Similarity 75.0
Matches 27; Conservative
                                                                                                                                                                             ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-130-645A-243478
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US-11-130-645A-385098
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LENGTH: 64
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Pred. No. 2.5e+03;
0; Mismatches 14; Indels (
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APPLICANT: Bentwich, Itzhak
APPLICANT: Amir, Avniel
APPLICANT: Yael, Karov
APPLICANT: Ranit, Aharonov
TITLE OF INVENTION: Micrornas and Uses Thereof
FILE REPERENCE: 06087.0202.020313
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PRIOR FILING DATE: 2005-05-14
PRIOR APPLICATION NUMBER: US 10/709,577
PRIOR APPLICATION NUMBER: US 10/709,577
PRIOR APPLICATION NUMBER: US 10/709,572
PRIOR FILING DATE: 2004-05-14
PRIOR FILING DATE: 2004-05-14
PRIOR FILING DATE: 2005-03-30
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APPLICATION NUMBER: US 60/662,742
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Best Local Similarity 68.2%;
Matches 30; Conservative (
                                                                                                                                                                                                                      TYPE: RNA
CORGANISM: Homo sapiens
US-11-130-645A-426292
SOFTWARE: Paten
SEQ ID NO 426292
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RESULT 12 US-11-130-645A-426292 ; Sequence 426292, Application US/11130645A

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TYPE: RNA
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NUMBER OF SEQ ID NOS: 760616
SOFTWARE: Patentin version 3.3
SEQ ID NO 660220
LENGTH: 64
                          PRIOR FILING DATE: 2005-01-06
PRIOR APPLICATION NUMBER: US 60/593,081
PRIOR PLING DATE: 2004-12-08
PRIOR FILING DATE: 2004-12-08
PRIOR FILING DATE: 2004-11-15
PRIOR FILING DATE: 2004-11-15
PRIOR FILING DATE: 2004-0-04
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 760616
SOFTWARE: PatentIn version 3.3
SEQ ID NO 641194
LENGTH: 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 66020. Application US/11130645A; Publication No. US20070050146A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Itzhak
APPLICANT: Amir, Avniel
APPLICANT: Ranit, Avniel
APPLICANT: Ranit, Avniel
APPLICANT: Ranit, Aranion
TILE OF INVENTION: Micrornas and Uses Thereof
FILE REFERENCE: 06097.0202. CPUS13
CURRENT FILING DATE: 2005-05-16
PRIOR PELING DATE: 2005-05-16
PRIOR PELING DATE: 2005-05-14
PRIOR PELING DATE: 2005-03-10
PRIOR PELING DATE: 2005-03-30
PRIOR PELING DATE: 2005-03-30
PRIOR PELING DATE: 2005-03-30
PRIOR PELING DATE: 2005-03-10
PRIOR PELING DATE: 2004-11-15
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Pred. No. 2.5e+03;
0; Mismatches 14.
APPLICATION NUMBER: US 60/593,329
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Best Local Similarity 68.2
Matches 30; Conservative
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; ORGANISM: Homo sapiens
US-11-130-645A-660220
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; ORGANISM: Homo sapiens
US-11-130-645A-641194
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APPLICANT: Behrunch, Inzhak
APPLICANT: Behrunch, Inzhak
APPLICANT: Anniel
APPLICANT: Ranir, Anniel
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APPLICANT: Ranir, Anniel
APPLICANT: Ranir, Anniel
TITLE OF INVENTION: Micrornas and Uses Thereof
FILE REFERENCE: 06087.0202.CPUS13
CURRENT PAPLICATION NUMBER: US/11/130,645A
CURRENT FILING DATE: 2005-05-16
PRIOR FILING DATE: 2006-05-14
PRIOR PILING DATE: 2004-05-14
PRIOR FILING DATE: 2004-05-14
PRIOR FILING DATE: 2004-05-14
PRIOR FILING DATE: 2004-05-14
PRIOR FILING DATE: 2005-03-30
PRIOR PLICATION NUMBER: US 60/665,094
PRIOR PLICATION NUMBER: US 60/652,742
PRIOR FILING DATE: 2005-03-30
PRIOR FILING DATE: 2005-03-17
PRIOR PLICATION NUMBER: US 60/593,081
PRIOR FILING DATE: 2006-01-06
PRIOR FILING DATE: 2004-11-06
PRIOR PLICATION NUMBER: US 60/522,457
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14 CUGGCCCCUUCCUAGGGUTAUGAGCUGGAACUGUUCUACUUUC 57
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US-11-130-645A-90177
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14; Indels

19.2 24.3 79 1 AIS39851 19 24.1 51 19 BX289701 19 24.1 65 11 EC687830 19 24.1 78 10 CR58713 19 24.1 79 15 AZ605020 18.8 23.8 46 1 AA569383 18.8 23.8 67 12 DY248960 18.8 23.8 67 12 DY248960 18.8 23.8 73 8 CD945332	18.6 23.5 37 15 A2769939 18.6 23.5 48 15 A276726 18.6 23.5 73 1 AA912015 18.6 23.5 73 12 EB98661 18.4 23.3 57 7 A1103010 18.4 23.3 50 7 A1103012 18.4 23.3 50 1 EC694167 18.4 23.3 70 11 EC69412	4.4 23.3 74 16 2.2 23.0 32 17 2.2 23.0 58 17 2.2 23.0 58 17 2.2 23.0 58 18 2.2 23.0 63 8 2.2 23.0 77 19 2.3 23.0 77 19 2.3 23.0 77 19 2.3 65 18	ALIGNMENTS	BX728792 BX728792 XGC-tadpole Xenopus tropmANA sequence. BX728792 BX728792.1 GI:38401533 BX788792.1 GI:38401533 Xenopus tropicalis (western clawe Xenopus tropicalis (western clawe Xenopus tropicalis Butaryota; Metazoa; Chordata; Cra Amphibia; Batrachia; Anura; Mesob Xenopodinae; Xenopus; Silurana.	REFERENCE 1 (bases 1 to 76) AUTHORS Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J. TITLE Sanger Xenopus tropicalis EST project 2001 (11_2003) JOURNAL Unpublished (2003) COMMENT Contact: Croning MDR Sanger Institute Hinxton, Cambridgeshire, CB10 1SA, UK Email: trop@sanger.ac.uk Sanger Xenopus tropicalis EST project 2001	TROPICALIS_SEQUENCE ID: TTPA036j08.plkSP6 Sequencing primer: SP6 This sequence is from a Xenopus Gene Collection (XGC) library constructed by Nigel Garrett. CDNA was oligod Trimed from Sug of poly A+ RNA from tadpole embryos. ECORI-NotI cut cDNA was then ligated into pCS107 with ECORI at the 5' end and NotI at the 3' end. Vector: pCS107; Site 1: ECORI; Site_2: NotI HOST: ESCHETICALIA coli DH10B. FEATURES 1. 76 /organism="Xenopus tropicalis" /mol type="MRNA" /db Xaref="taxon:8364" /clone="TTPA036j08"
GenCore version 6.2.1 Copyright (c) 1993 - 2007 Biocceleration Ltd. OM nucleic - nucleic search, using sw model Run on: June 19, 2007, 14:05:10; Search time 2495 Seconds (without alignments)	canca 7	Total number of hits satisfying chosen parameters: 624300 Minimum DB seq length: 0 Maximum DB seq length: 80 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database: EST:*	2: gb_est3:* 4: gb_est4:* 5: gb_est6:*	6: gb htc:* 7: gb est2:* 8: gb_est2:* 9: gb_est3:* 10: gb_est3:* 11: gb_est12:* 13: gb_est11:* 14: gb_est10:* 15: gb_gss1:* 16: gb_gss2:* 17: gb_gss2:* 18: gb_gss2:* 19: gb_gss3:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES Result Query No. Score Match Length DB ID	21.6 27.3 76 5 BX728792 20.6 26.1 76 12 EC019237 19.8 25.1 78 19 CT351516 19.4 24.6 71 13 CW026424 19.4 24.6 71 13 DN441479 19.4 24.6 76 16 BZ381406 19.4 24.6 77 11 BZ881406 19.4 24.6 78 11 BZ8813 19.4 24.6 78 11 BZ8813 19.2 24.3 46 1 AI360975 19.2 24.3 56 17 CW022621 19.2 24.3 78 18 DX045680

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Mus musculus
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Baille,M., Cheung,L., Chong,A., Goldschmidt,S., Hussain,S.,
Laufer,A., Oliva,J., Murray,L., Park,C., Reyes,J., Wong,M.,
Milash,B., Amundsen,C., Orton,A., Shao,A., Platt,D., Swimmer,C. and
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/dev stage="tadpole (stage 35-40)"
/lab_host="E. coli DH10B"
/clone lib="XGC-tadpole"
/note="vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from tadpole
embryos. EcoRI-NotI cut cDNA was then ligated into pCS107
with EcoRI at the 5' end and NotI at the 3' end"
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Sus scrofa genomic clone CH242-438014, genomic survey sequence.
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Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
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                                                                                                                                                   27.3%; Score 21.6; DB 5; Length 76;
41.7%; Pred. No. 1.8e+04;
Live 12; Mismatches 9; Indels
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6705 Odyssey Drive, Huntsville, AL 35806, USA
Email: KSCHMITT@OPENBIOSYSTEMS.COM.
Location/Qualifiers
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/mol_type="mkNA"

/mol_type="mkNA"

/mol_type="taxon:6239"

/clone="1768654"

/clone_lib="KZ41"
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EC019237.1 GI:103033970
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Contact: Karin Schmitt
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Caenorhabditis elegans
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Campus, Hinkton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 438014. 438014
is part of the CMORI-242 BAC Library created by P. de Jong. Further details: http://www.aanger.ac.uk/Projects/S_scrofa/.
                                                                                                                   Humphray, S.J., Plumb, R.W. and Durham, J.L.
Direct Submission
Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome.
Campus, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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1 (bases 1 to 71)
Cobellis, G. Nicolaus, G., Iovino, M., Romito, A., Marra, E.,
Cobellis, M., Sardiello, M., Di Giorgio, F.P., Iovino, N., Zollo, M.,
Ballabio, A. and Cortese, R.
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Tel: +390816132205
Fax: +390815790919
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Nucleic Acids Res. 33 (4), e44 (2005)
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/note="Vector pTARBAC1.3_BamHI
sex female"
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/cell_type="Embryonic stem cell"
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/mol_type="mRNA"
/strain="129 ola"
                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Sus scrofa"
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/clone="CH242-438014"
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/clone="A011.G4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CW020424
CW020424.1 GI:52789684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18; Conservative
                                                                                                (bases 1 to 78)
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BZ381406 10.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_116666.43.10.x, genomic
                                                                                                         /tissue_type="kidney"
/lab host="DH10B"
/clone lib="LIB5338"
/note="Vector: pSPORT1; Site_1: Sal1; Site_2: Not1; whole organ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="SALK list666.43.10.x"
/clone="SALK list666.43.10.x"
/clone="Ib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 76)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Adorniab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At5g61190 Class: TDNA tagged.
                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                 57
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0
                                                                                                                                                                                                                                                                                                                                                 5 GCCGCGCGCAGACGACCGCCCCCCTTAAUUGUACUUCGGGCUCGUAU
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                                                                                                                                                                                                                                                            Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
1181: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.6%; Score 19.4; DB 16; 37.7%; Pred. No. 1e+05; tive 12; Mismatches 21;
                                                                                                                                                                                                                                                              Score 19.4; DB 13;
                                                                                                                                                                                                                                                                               Pred. No. 1e+05;
8; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Arabidopsis thaliana"

    .71
    /organism="Canis familiaris"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/ecotype="Col-0"
                                           /mol_type="mRNA"
/db_xref="taxon:9615"
/clone="CLN14241789"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BZ381406.1 GI:25475317
                                                                                                                                                                                                                                                         ch 24.6%;
1 Similarity 45.3%;
24; Conservative 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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BZ381406
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Best Local Similarity
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Best Local S:
Matches 24,
        source
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LOCUS
DEFINITION
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SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J., and Bradley, A.
                                                                                                                                                                                                                                                                                                                                                 GSS 05-JUL-2004
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Mammalia, Eutheria, Laurasiatheria, Carnivora, Caniformia, Canidae,
                                                                                                                                                                                                                                                                                                                                             CR076775

Reverse strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHPP113c17, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
1 (bases 1 to 58)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER Location/Qualifiers
                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 bp mRNA linear EST (LIB5338-102-A1-K2-G6 LIB5338 Canis familiaris cDNA clone CLN14241789, mRNA sequence.
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                                                                                                                                                                                                1 GGAGGGCGGGGGAGAGAGGGGCUCUGGCCCCUUAAUUGUACUUCGGG 50
                                                                                                             24.8%; Score 19.6; DB 17; Length 71; 52.0%; Pred. No. 8.7e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.6%; Score 19.4; DB 19; Length 58; 75.9%; Pred. No. 1e+05;
                                                                                                                                                       Indels
/cell_line="E14"
/clone_lib="TIGEM gene trap library"
/note="Vector: pFLIP1"
                                                                                                                                                       19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                       5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Nick Staten
Tel: 636 247 6855
Email: nicholas.r.staten@pfizer.com.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSS; genome survey sequence; MICER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPP113c17"
/clone_lib="MHPP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission (Staten, N.R.)
Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                  CR076775.1 GI:49810363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DN441479.1 GI:60637724
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Canis familiaris
                                                                                                                                                       26; Conservative
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tes 22; Conserv
                                                                                                                                 Similarity
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                                                                                                             Query Match
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CR076775
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DN441479
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SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL PUBMED

COMMENT

DEFINITION

CW236987

RESULT

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ACCESSION

VERSION KEYWORDS

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EC034520 78 bp mRNA linear EST 26-MAY-2006
4005308 KZ41 Caenorhabditis elegans cDNA clone 1779480, mRNA
                   Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h LLNL ; contact the further information.
                                                                Catarrhini; Hominidae; Homo.

1 (bases 1 to 78)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Helman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euarchontoglires; Primates; Haplorrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 CGAGCGGCUCUGGCCCCUUJAAUUGUACUUCGGGCUCGUAUUGUCUCCUUUCGCC
                                                                                                                                                                                                                                                  Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 11; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLLL
This clone is available royalty-free through LLL
IMAGE Consortium (info@image.llnl.gov) for furth
Trace considered overall poor quality
Trace considered overall poor quality
Seq primer: Promega -21ml3
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.6%; Score 19.4; DB 11;
41.1%; Pred. No. 1e+05;
tive 9; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/clone="IMAGE:161634"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="GDB:575803"
                       Chordata;
                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
Insert Size: 826
                                                                                                                                                                                                                           The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EC034520.1 GI:103065021
                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 78)
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Matches 23; Conserv
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ORGANISM
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EC034520
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                                                                                                                                     CW236987 1015918_116_37515_093 Sorghum methylation filtered library (LibID: 104) Sorghum bethylation filtered library (LibID: 104) Sorghum bicolor genomic clone 11215918, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to Ek fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."
                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
Clade, Panicoideae, Andropogoneae, Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Sorghum methylation filtered library (LibID: 104)"
                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 76)
Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D., Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K., McMenamy, J., Smith, M., Holeman, H., Roe, B.A, Wiley, G., Korf, I.F., Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A. and Martienssen, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 bp mRNA linear EST 10-JUL-
y149910.s1 Scares breast 3NbHBst Homo sapiens cDNA clone
IMAGE:161634 3' similar to gb:J02611 APOLIPOPROTEIN D PRECURSOR
(HUMAN);, mRNA sequence.
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                       56
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GAGACTGCAAGCTGTACAATTGTTTCTCTTGGTTGTTGTTTTTTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sorghum genome sequencing by methylation filtration
PLoS Biol. 3 (1), e13 (2005)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Bedell JA
Orion Genomics, LLC.
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ...76
'organism="Sorghum bicolor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 314 615 5975
Email: jbedell@oriongenomics.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'mol_type="genomic DNA"
'cultivar="ATx623"
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Location/Qualifiers
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Sorghum bicolor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
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Fax: 81-3-5449-5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Conservative
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Zeng,K., Garrick,B., Chen,F., Gnirke,A., Swan,K., Bjerke,L.,
Baille,M., Cheung,L., Chong,A., Goldschmidt,S., Hussain,S.,
Laufer,A., Oliva,J., Murray,L., Park,C., Reyes,J., Wong,M.,
Milash,B., Amundsen,C., Orton,A., Shao,A., Platt,D., Swimmer,C. and
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
Gound through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
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Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Haplorhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Catarrhini, Hominidae, Homo.

(Catarrhini, Hominidae, Homi
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/tissue_type="glioblastoma (pooled)"
/lab_hogt="DH108"
                                                                                                                                                                                                                                     Exelixis Caenorhabditis elegans EST project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Caenorhabditis elegans"
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Insert Length: 771 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:6239"
/clone="1779480"
/clone_lib="KZ41"
                                                                                                                                                                                                                                                                               Unpublished (2006)
Contact: Karin Schmitt
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AI360975
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50 bp mRNA linear EST 18-ADR-2006
AU105862 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HS107994 5', mRNA sequence.
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Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Sataki, Y., Nota, T., 18ogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                                                                                                                                                                                                                                                                                        24.3%; Score 19.2; DB 1; Length 46; 75.0%; Pred. No. 1.1e+05; rive 0; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                     13 AGGGGGGGAAAGACCAGGGGCCCAACCCCC 44
                                                                                                                                                                                                                                                                                                                                                                                          3 AGGCCGGCGAGAGACGAGCGGCUCUGGCCCC 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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Fri

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Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
    Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Hahn,J.H. and Park,B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone Unpublished (2005)
                                                                                      Conteact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Pax: +82-31-299-1672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                         KBrB047B02
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DEFINITION
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DX045680 10-JAN-2006 KBFB047B02R KBFB BAC 11brary Brassica rapa subsp. pekinensis genomic clone KBFB047B02, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
      W022621 68 28-OCT-2004 10431956 1 30008 Sorghum methylation filtered library (LibID: 104) Sorghum bicolor genomic clone 10431956, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 78)
Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M.,
                                                                                                                                                                                                          Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  colone="10431956"
clone_lib="Sorghum methylation filtered library (LibID:
                                                                                                                                                                                                                                                                                1 (bases 1 to 66)
Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,
Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K.,
MCMenamy, J., Smith, M., Holeman, H., Roe, B.A, Wiley, G., Korf, I.F.,
Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A. and
Martienssen, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                              Sorghum genome sequencing by methylation filtration PLoS Biol. 3 (1), e13 (2005) 15660154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 CGGGCATCTTTATACCCCTAATTCTACTTCGGACACTTGT 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 24.3%; Score 19.2; DB 17; Best Local Similarity 42.5%; Pred. No. 1.2e+05; Matches 17; Conservative 10; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: jbedell@oriongenomics.com
Plate: 162 row: b column: 12
Seg primer: M13(40) Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 66.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class: methylation filtered
                                                                                                                                                                       Sorghum bicolor (sorghum)
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                                                                                                      CW022621
CW022621.1 GI:54699354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99. .
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AUTHORS
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DX045680
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VERSION
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JOURNAL
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AUTHORS
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Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing Dy: Washington University Genome. Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E., Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                            /lab host="E.coli DH10B"
/clone lib="KBrB, Brassica rapa BamHI BAC library"
/clone lib="KBrB, Brassica rapa BamHI; Brassica rapa spp
/note="Vector: Chiftu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALSJYBS1 TOT CGAP UT3 HOMO SADIONS CDNA LINEAR EST 13-MAY-1999 tp65£05.X1 NCI CGAP UT3 HOMO SADIONS CDNA Clone IMAGE:2204193 3' similar to SW:\(\bar{P}\)F111_\(\bar{P}\)IG P51524 PROPHENIN-1 PRECURSOR ; contains L1.b1 ALSJ9851
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Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
                      pekinensis BamHI BAC clone
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1 (bases 1 to 79)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 78;
                                                                                                                                                                                                            /organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 24.3%; Score 19.2; DB 18; Best Local Similarity 40.0%; Pred. No. 1.2e+05; Matches 16; Conservative 11; Mismatches 13;
                               rapa ssp.
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Insert Length: 1117 Std Error: 0.00
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                       /sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB047B02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 1
Email: pbeom@rda.go.kr
BAC end sequence of Brassica
                                                                                                                                                       Location/Qualifiers
                                                                                              Seq primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI539851.1 GI:4453986
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Query Match

24.3%; Score 19.2; DB 1; Length 79;

Best Local Similarity 39.1%; Pred. No. 1.2e+05;

Matches 25; Conservative 11; Mismatches 28; Indels 0; Gaps 0;

Qy 7 CGGGGGAGAGACGGCUCUGGCCCUUAAUUGUACUUCGGCCUCUAUUGUCUCUCC 66

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Oy 67 UUUC 70

:: | 5 TTCC 2

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Search completed: June 19, 2007, 15:23:11 Job time : 2499 secs AX649755 Sequence
A2430 LST3 primer
AR010021 Sequence
AR034756 Sequence
12444 Sequence
12444 Sequence
BD268715 Inhibitor
CQ764654 Sequence
AR229112 Sequence
AR229112 Sequence
AR23172 Sequence
AR304584 Sequence
AR30459 Sequence
AR317580 Sequence
AR317580 Sequence
AK69749 Sequence
AK69749 Sequence
CS113604 Sequence
BD411373 Method fo
CS113604 Sequence
DD023799 YEAST-BAS
12640 Sequence
BD345059 Antisense
CS117222 Sequence
BD345059 Antisense
CS117222 Sequence

AX64977 AX64977 AX01007 AR03477 124749 AX2291 AR2291 AR30453 AR30453 AR30453 AR30453 AR30453 AR30453 AR504974 AX64974	AX46967 BD34509 CG1767 AR88233 AX19183	linear	; Length 24; 4; Indels 0 linear PA
200 200 200 200 200 200 200 200 200 200	13.4 55.8 17 2 13.4 55.8 18 2 13.4 55.8 18 2 13.4 55.8 18 2 13.4 55.8 18 2	24 bp DNP equence 20 from patent US 5756684. [101008	Query Match 65.0%; Score 15.6; DB 2
ncore version 6.2.1 1993 - 2007 Biocceleration Ltd. Ing sw model 12:41:00 ; Search time 1106 Seconds (without alignments) 1499.898 Million cell updates/sec 1499.898 Million cell updates/sec s136 ucgccaccuc 24 chosen parameters: 2038054	į es	results predicted by chance to have a l to the score of the result being printed, of the total score distribution.	Description AR010008 Sequence AR01476 Sequence AR03476 Sequence 12475 Sequence 3 12475 Sequence 12477901 Sequence AR877901 Sequence AR877901 Sequence 126407 Sequence 12640750 Sequence 12640751 Sequence AK649751 Sequence AK649753 Sequence AK649753 Sequence AK649753 Sequence AK649753 Sequence
Gepyright (c) search, us: 19, 2007, : 19, 2007, : 19, 2007, : 11TY_NUC 2 10-0, Gal 341 seqs, 34 satisfying	length: 0 length: 25 g: Minimum Match 0% Maximum Match 100% Listing first 45 summaries GenEmbl:*	gD_pat:* gD_ph:* gD_ph:* gD_ph:* gD_pr:* gD_ro:* gD_vi:* gD_vi:* gD_no:* gD_no:* gD_no:* gD_no:* gD_no:* gD_no:* gD_no:* gD_no:* gD_no:* gD_no:*	tch Length DB ID 5.0 24 2 AR010008 5.0 24 2 AR034740 5.0 24 2 AR034740 5.0 24 2 AR034740 5.0 24 2 AR0347903 5.0 24 2 AR0347903 6.0 24 2 AR077901 6.0 24 2 AR077901 6.0 24 2 AR077901 7.2 2 2 AR077901 7.2 2 2 AR077901 7.2 2 2 AR077905 7.3 2 2 AR077905 7.4 2 AR077905 7.5 2 2 AR077905 7.6 2 2 2 AR077905 7.7 2 2 2 AR07779 7.7 2 2 2 AR07777 7.7 2 2 2 AR07775 7.7 2 2 2 AR07777 7.7 2 2 2 AR0777 7.7 2 2 2 AR077 7.7 2 2 AR077 7.7 2 2 AR077 7.
eic - nucle Ju score: 24 score: 24 table: ID table: IG annber of hi	Minimum DB seq leng Maximum DB seq leng Post-processing: Mi Mi Database: Ge	2:: 2:: 3:: 4:: 10:: 11:: 11:: 11:: 12:: 13:: 14:: 16:: 16:: 16:: 16:: 16:: 16:: 17:: 18:: 18:: 18:: 18:: 18:: 18:: 18	Result Query No. Score Match 1 15.6 65.0 2 3 15.6 65.0 4 15.6 65.0 5 5 15.6 65.0 7 15.2 63.3 9 14.4 60.0 10 14.4 60.0 11 14.2 59.2 13 14.2 59.2 14 14.2 59.2 15 14.2 59.2 16 14.2 59.2 17 14.2 59.2 18 14.2 59.2 18 14.2 59.2

PAT 04-DEC-1998

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Gaps

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PAT 04-DEC-1998

PAT 07-0CT-1996

TITLE JOURNAL

FEATURES

ORIGIN

Matches

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1 (bases 1 to 21)
Allawi,H., Bartholomay,C.T., Chehak,L., Curtis,M.L., Eis,P.S.,
Hall,J.G., Ip,H.S., 'Kaiser,M., Kwiatkowski,R.W. Jr., Lukowiak,A.A.,
                                                                                                                                                                                                                                                                                                                         Length 24;
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50.0%; Pred. No. 2e+04;
tive 7; Mismatches 4;
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Sequence 2144 from patent US 7045289.
AR877903.1 GI:111975391
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Johnson, E.W. and Bergmann, A.D.
Cloning and expression of pur protein
Patent: US 5545551-A 3 13-AUG-1996;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Johnson, B. M. and Bergmann, A.D. Cloning and expression of pur protein Patent: US 5545551-A 15 13-AUG-1996; Location/Qualifiers
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124752
124752.1 GI:1604622
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/organism="unknown"
/mol_type="unassigned DNA"
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/organism="unknown"
/mol_type="unassigned DNA"
                                                24 bp
Sequence 3 from patent US 5545551
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Best Local Similarity 50.0%; Pred. No. 2e+04;
Matches 11; Conservative 7; Mismatches 4; Indels
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Johnson, E.M. and Bergemann, A.D.
Monoclonal antibodies to the pur protein
Patent: US 5869622-A 38 09-FEB-1999;
Location/Qualifiers
                                                                                                                   ch 65.0%; Score 15.6; DB 2; Score 15.0; DE 2; Similarity 50.0%; Pred. No. 2e+04; 11; Conservative 7; Mismatches 4;
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Johnson, E.M. and Bergemann, A.D.
Monoclonal antibodies to the pur protein
Patent: US 5869622-A 20 09-FEB-1999;
Location/Qualifiers
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Cloning and expression of PUR protein Patent: US 5756684-A 38 26-MAY-1998; Location/Qualifiers
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AR034760
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Sequence 20 from patent US 5869622.
AR034743
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/mol_type="unassigned DNA"
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2 TTTTCTCTCCTCCACCACCTC 23
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60.0%; Score 14.4;
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Location/Qualifiers
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3 CTCCTTTCCCCACCTC 18
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Allawi,H., Bartholomay,C.T., Chehak,L., Curtis,M.L., Eis,P.S.,
Hall,J.G., Ip,H.S., Kaiser,M., Kwiatkowski,R.W. Jr., Lukowiak,A.A.
Lyamichev,V., Ma,W., Olson-Munoz,M.C., Olson,S.M., Schaefer,J.J.,
Skrzypczynski,Z., Takova,T.Y., Vedvik,K.L., Lyamichev,N. and
Neri,B.P.
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Prockop, D.J., Ala-Kokko, L., Williams, C.J., Ritvaniemi, P.,
Prockop, D.J., Ala-Kokko, L., Milliams, C.J., Ritvaniemi, P.,
Bridwin, C., Hopkinson, I. and Ahmad, N. Nina.
Primers and methods for detecting mutations in the procollagen II
gene (COL2AI) that indicate a genetic predisposition for a
COL2AI-associated disease
Lyamichev, V., Ma, W., Olson-Munoz, M.C., Olson, S.M., Schaefer, J.J., Skrzypczynski, Z., Takova, T.Y., Vedvik, K.L., Lyamichev, N. and
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                                        Detection of RNA Sequences
Patent: US 7045289-A 2144 16-MAY-2006;
Third Wave Technologies, Inc.; Madison, WI;
US;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Third Wave Technologies, Inc.; Madison, WI;
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50.0%; Pred. No. 3.1e+04;
iive 7; Mismatches 3;
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Sequence 99 from patent US 5948611.
AR072296
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/organism="unknown"
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Allawi, H., Bartholomay, C.T., Chehak, L., Curtis, M.L., Eis, P.S., Hall, J.G., Ip, H.S., Kaiser, M., Kwiatkowski, R.W., Jr., Lukowiak, A.A., Lyamichev, V., Ma, W., Olson-Munoz, M.C., Olson, S.M., Schaefer, J.J., Skrzypczynski, Z., Takova, T.Y., Vedvik, K.L., Lyamichev, N. and
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Prockop, D.J., Ala-Kokko, L. and Ritvaniemi, P.
Princkop, D.J., Ala-Kokko, L. and Ritvaniemi, P.
Primers and methods for detecting mutations in the procollagen II
gene that indicate a genetic predisposition for osteoarthritis
Patent: US 5558988-A 99 24-SEP-1996;
Location/Qualifiers
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                                                                                                          Score 14.4; DB 2;
Pred. No. 7.1e+04;
5; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detection of RNA Sequences
Patent: US 7045289-A 2146 16-MAY-2006;
Third Wave Technologies, Inc.; Madison,
US;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 bp DNA
US 7045289.
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Sequence 99 from patent US 5558988.
126407
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/organism="unknown"
/mol_type="unassigned DNA"
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1. .18
/organism="unknown"
/mol_type="unassigned
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/organism="unknown"
                                                                                          60.0%; Scur.
62.5%; Pred
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Sequence 2146 from patent
AR877905
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Gaps

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SOURCE ORGANISM

REFERENCE AUTHORS

RESULT 12 128585/c

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TITLE JOURNAL FEATURES

ORIGIN

PAT 22-MAR-2003

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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Haplorrhini,
Catarrhini, Hominidae, Homo.
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Patent: EP 1273660-A 1591 08-JAN-2003;
                                                                                                           Human sodium-hydrogen exchanger like protein 1
Patent: EP 1273660-A 1590 08-JAN-2003;
Aeomica, Inc. (US)
Location/Qualifiers
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Pred. No. 8.9e+04;
6; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 bp Di
Sequence 1591 from Patent EP1273660.
AX649751
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Best Local Similarity 52.6%;
Matches 10; Conservative
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Homo sapiens (human)
Homo sapiens
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59.2%; Score 14.2; DB 2;
Best Local Similarity 36.8%; Pred. No. 8.8e+04;
Matches 7; Conservative 9; Mismatches 3;
     Pred. No. 7.1e+04;
6; Mismatches 1
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Sequence 1590 from Patent EP1273660.
AX649750
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Watanabe K.A., Ren,W.-Y. and Weil,R.
Complementary DNA and toxins
Patent: US 5652350-A 38 29-UUL-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                      1 (bases 1 to 21)
Watanabe,K.A., Ren,W.-Y. and Weil,R.
Complementary DNA and toxins
Patent: US 5571937-A 38 05-NOV-1996;
Location/Qualifiers
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Sequence 38 from patent US 5652350.
158747
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Sequence 38 from patent US 5571937.
128585
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19 TTTATCTCTCCTTTCTCC 1
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      Similarity 56.2%;
9; Conservative
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19 GTCTCTTTTGCCA 4
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        Best Local
Matches
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AX649750/C
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PAT 22-MAR-2003

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AX649750.1 GI:29152568

6.2.1	Biocceleration Ltd.
version	- 2007
GenCore	c) 1993
•	Copyright (

OM nucleic - nucleic search, using sw model

Run on:

June 19, 2007, 12:28:50 ; Search time 246 Seconds (without alignments) 721.516 Million cell updates/sec

US-10-604-726A-5136 24 Title: Perfect score:

1 uauugucucuccuuucgccaccuc 24 Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

5620219 segs, 3705283702 residues Searched:

4355164 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 25

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn1990s:* N_Geneseq_200701:* Database :

geneseqn2003ds:* geneseqn2004as:* geneseqn2003cs: geneseqn2002as: geneseqn2001as: geneseqn2001bs: geneseqn2002bs: geneseqn2003as: geneseqn2003bs geneseqn2000s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004bs:*

geneseqn2005s:* geneseqn2007s:*

geneseqn2006s:

SUMMARIES

Description	Aad21686 Imperfect	Aaq44801 Purine-ri	Aaq44806 Oligonucl	Aat99274 Human PUR	Aav31726 Nucleotid	Aav31731 Nucleotid	Aax04070 Oligonucl	Aax04075 Oligonucl	Aee94315 3' primer	Adi94591 Murine IF	Adi94589 Murine IF	Aaq65826 Type II p	Adi94593 Murine IF	Aaq85989 S.tuberos	Aax56946 HIV-1 pro	Aef13105 Human mut	Adc05103 Human Na/
OI	AAD21686	AAQ44801	AAQ44806	AAT99274	AAV31726	AAV31731	AAX04070	AAX04075	AEE94315	ADI94591	ADI94589	AAQ65826	ADI94593	AAQ85989	AAX56946	AEF13105	ADC05103
98	4	~	7	7	7	~	7	7	15	7	7	7	7	7	~	12	10
% Query Match Length DB	24	24	24	24	24	24	24	24	25	21	22	18	20	23	21	21	25
% Query Match	65.8	65.0	65.0	65.0	65.0	65.0	65.0	65.0	65.0	63.3	63.3	60.09	0.09	0.09	59.2	59.2	59.5
Score	15.8	15.6	15.6	15.6	15.6	15.6	15.6	15.6	15.6	15.2	15.2	14.4	14.4	14.4	14.2	14.2	14.2
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Adc05104 Human Na/	Adc05109 Human Na/	Adc05105 Human Na/	Adc05108 Human Na/	Adc05106 Human Na/	Adc05107 Human Na/		Aaq44802 Oligonucl		Aav31727 Nucleotid	Aax04071 Oligonucl	Aah48099 Phytochro	Aec26021 Human all	Aec28387 Human all	Ack16088 Human mic	Adc03597 Human Na/	Aax94034 PCR prime	Abx04519 Human adi	Adc01938 Human zsi	Aad59884 ZC13641 o			Adj96212 Primer 2C	Adm72676 Human TAS	Aci35264 Human mic	Aci37022 Human mic	Aci92741 Human mic	Adc05102 Human Na/
ADC05104	ADC05109	ADC05105	ADC05108	ADC05106	ADC05107	AAQ38850	AAQ44802	AAT99270	AAV31727	AAX04071	AAH48099	AEC26021	AEC28387	ACK16088	ADC03597	AAX94034	ABX04519 ·	ADC01938	AAD59884	ADF18008	ACD02558	ADJ96212	ADM72676	ACI35264	ACI37022	ACI92741	ADC05102
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25	25	25	25	25	25	24	24	24	24	24	24	24	24	25	17	20	20	20	20	20	20	20	21	52	25	25	25
59.2	59.2	59.2	59.2	59.2	59.2	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	57.5	57.5	57.5	57.5	•	57.5	57.5	57.5	7	57.5	57.5	57.5	57.5
14.2	14.2	14.2	14.2	14.2	14.2	14	14	14	14	14	14	14	14	14	13.8	13.8	13.8	13.8	13.8	13.8	13.8	13.8	13.8	13.8	13.8	13.8	13.8
18	19	20	21	22	23	24	52	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

Imperfect direct repeat #1 of human RPGR exon ORF15 repetitive sequence. 686/c AAD21686 standard; DNA; 24 BP. 28-JAN-2002 (first entry) AAD21686; AAD21686/

Human; mutation; retinitis pigmentosa GTPase regulator; RPGR; genotyping; open reading frame; ORF; X-linked retinitis pigmentosa; XLRP; gene therapy; screening; forensic analysis; ds.

Homo sapiens.

WO200177380-A2.

18-OCT-2001.

10-APR-2001; 2001WO-GB001622.

10-APR-2000; 2000GB-00008801.

(MEDI-) MEDICAL RES COUNCIL

Wright A;

WPI; 2001-663057/76.

Diagnosing disease or predisposition to disease, associated with disease causing mutations in retinitis pigmentosa GTPase regulator gene by genotyping ORF15 of the gene, and determining presence of mutations.

Disclosure, Fig 4E; 100pp; English.

The present invention relates to a method for diagnosing disease or predisposition to a disease, associated with a disease causing mutations in a retinitis pigmentosa GTPase regulator (RPGR) gene involves genotyping a RPGR gene, and determining whether the genotype comprises a

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disease causing mutations, where the risk genotype is present within open detecting frame (ORF)15 of the RPGR gene. The method is useful for detecting a certain disease state e.g., X-linked retinitis pigmentosa (XLRP). The kit is useful for detecting and measuring disease causing mutations in biological fluids and tissues and for localising mutation in tissues. The mutant RPGR gene is useful in gene therapy techniques and for screening agents capable of affecting the expression of the sequences and/or the biological activity of mutant RPGR. They are preferably useful for identifying agonists and antagonists of RPGR. The mutant RPGR gene is also useful in identification of potential pharmacoutical targets in high throughput screening assays and forensic analysis. The present sequence is the imperfect direct repeat of human RPGR exon ORF15 repetitive DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cloning and expression of PUR protein, involved in regulation of DNA replication - also oligo:nucleotide(s) and antibodies for use in the treatment of proliferative diseases, e.g. cancer.
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single-strand binding protein; PUR protein; cellular oncogene; eukaryotic origin of replication; gene amplification; cancer cell; retinoblastoma protein; helix-destabilising protein; inhibitor;
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                                                                                                                                                                                                                                    Score 15.8; DB 4; Length 24; Pred. No. 3.9e+03;
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nilarity 52.6%;
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(first entry)
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02-FEB-1993;
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28-SEP-1994
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PUR elements are purine-rich 24 nucleotide DNA sequences which occur at eukaryotic origins of replication and 5' flanking regions of some cellular oncogenes. The PUR protein (AARS0310) was originally identified as a 27kD HeLa cell nuclear factor that bound in a sequence-specific manner to a major site of DNA bending located 1.6kb.upstream of the transcription start site of the human c-myc gene; the site recognised by PUR protein had the sequence AAQ44801. (Updated on 25-MAR-2003 to correct

Claim 6; Page 65; 97pp; English.

Sequence 24 BP; 8 A; 0 C; 14 G; 2 T; 0 U; 0 Other;

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sequence element found 1.6kb upstream of the cellular c-myc gene. The PUR element (see AAQ4801) is located in a region of DNA bending activity which is a structural feature often associated with origins of DNA creplication. The PUR protein AAR50310 binds to the PUR element. (Updated on 25-MAR-2003 to correct PN field)
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                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide MR0700 used in characterising c-myc PUR element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single-strand binding protein; PUR protein; cellular oncogene; eukaryotic origin of replication; gene amplification; cancer certinoblastoma protein; helix-destabilising protein; inhibitor;
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   Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24 BP; 2 A; 14 C; 0 G; 8 T; 0 U; 0 Other;
Score 15.6; DB 2;
Pred. No. 4.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Mismatches
                                                               7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SINAI SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24
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                                                                                                                         3 UNGUCUCUCCUUUCGCCACCUC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 37; 97pp; English.
                                                                                                                                                           rrrcrcrccrccaccaccrc 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 ungueneconnecededecacene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hyperproliferation; c-myc; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93WO-US008102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92US-00938189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-00014943
      65.0%;
50.0%;
                                                                                                                                                                                                                                                                                                                                  AAQ44806 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT99274 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Johnson EM, Bergemann AD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 50.0
Matches 11; Conservative
                                                               11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1994-101114/12
   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNUOM ( NUOM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9405689-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
28-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-MAR-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT99274;
                                                                                                                                                                                                                                                                                                                                                                                            AAQ44806;
                                                                                                                                                                                   23
                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT99274
ID AAT9
XX
AC AAT9
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IID AAQ44806

AAC AAQ4

XX AA
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                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                셤
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protein and its fragments - that inhibit PUR protein binding to PUR
                                                                                                                                                                               the invention, involving the use of the PUR protein and its fragments, which inhibit PUR protein binding to PUR element or other proteins. Inhibitors of PUR activity may be useful for treating viral infections
                                                                                                                                                                   This is the nucleotide sequence of the PUR element used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUR-alpha gene; inhibition; viral infection; cancer; PUR element; hyperproliferative disease; ss.
                                                                                                                                                                                                                                                    Sequence 24 BP; 8 A; 0 C; 14 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleotide sequence of the oligonucleotide MR0700,
                                                                                                                                                                                                                          and hyperproliferative diseases such as cancer
                                                                                                                                                                                                                                                                    65.0%; Sco. 50.0%; Pred. No. 4...
             (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SINAI SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                      3 UNGUCUCUCCUUUCGCCACCUC 24
                                                                                                                                       Disclosure, Col 12; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                      95US-00470911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92US-00938189
93US-00014943
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV31731 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-SEP-1998 (first entry)
                                        Johnson EM;
                                                                                                             element or other proteins,
                                                                                                                                                                                                                                                                                                           11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-321632/28
                                                                   WPI; 1998-321632/28
                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNUOM ( NUOM)
                                        Bergemann AD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bergemann AD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US5756684-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV31731;
                                                                                                                                                                                                                                                                                                                                                                  23
                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUR
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                    The probes AAT99270-T99277 were used to screen for positive clones containing a 467 bp Sau3AI fragment of the human c-myc upstream region cloned into pUC19. Isolated sequences were then used as probes to screen an expression library for sequences encoding the PUR protein. The PUR sequence can be used to identify chemical or biological compounds that bind to PUR or binding fragments of PUR. Inhibitors of PUR activity may
                                                                                                                                                                                                                                                                                                                                                                  Assays for PUR protein ligands or modulators - using immobilised PUR protein or fragments, to treat hyper-proliferative diseases, e.g. cancer
                                                    FUR element; human; c-myc; inhibitor; hyperproliferative disease; ss; cancer; probe; hybridisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inhibition; viral infection; cancer; PUR element; ive disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be used to treat hyperproliferative diseases such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 65.0%; Score 15.6; DB 2; Length 24; Best Local Similarity 50.0%; Pred. No. 4.8e+03; Matches 11; Conservative 7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 24 BP; 2 A; 14 C; 0 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence of the PUR element
                                                                                                                                                                                                                                                                                 SINAI SCHOOL MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTTCTCTCCCTCCACCACCTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNGUCUCUCCUTUCGCCACCUC 24
                           Human PUR-alpha gene probe MR0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                                                                                                                                                            Example; Col 26; 64pp; English
                                                                                                                                                                                                                        92US-00938189.
93US-00014943.
95US-00470911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                                              95US-00486421.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUR-alpha gene; inhibition;
hyperproliferative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV31726 standard; DNA; 24
                                                                                                                                                                                                                                                                                                            Johnson EM;
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                        WPI; 1997-488859/45
                                                                                                                                                                                                                                                                                 INDOM ( NDOM)
                                                                                                                                                                                                                                                                                                            Bergemann AD,
                                                                                                               Homo sapiens
                                                                                                                                                                                              17-JUN-1995;
                                                                                                                                                                                                                          28-AUG-1992;
                                                                                                                                                                                                                                        32-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-AUG-1992;
02-FEB-1993;
                                                                                                                                                                                                                                                       36-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-SEP-1998
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15-APR-1998
                                                                                                                                         JS5672479-A.
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                                                                                                                                                                    30-SEP-1997
                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV31726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV31726/c
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Gaps

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Indels

BP

Length 24;

6; DB 2; 4.8e+03;

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This is the nucleotide sequence of an oligonucleotide used in the method of the invention, involving the use of the PUR protein and its fragments, which inhibit PUR protein binding to PUR element or other proteins. Inhibitors of PUR activity may be useful for treating viral infections and hyperproliferative diseases such as cancer
protein binding to PUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24 BP; 2 A; 14 C; 0 G; 8 T; 0 U; 0 Other;
protein and its fragments - that inhibit PUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.0%; Score 15.6;
                                                                                                                         Example 6.1.1; Col 27; 63pp; English.
                                               element or other proteins
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RESULT 7 AAX04070/c

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The present invention describes a monoclonal antibody that specifically binds to an epitope of the PUR protein. Antibodies that bind to the PUR protein and neutralise PUR activity may be used to treat hyperproliferative diseases such as cancer. PUR antibodies may be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hyperproliferative diseases such as cancer. PUR antibodies may be used diagnostically to detect aberrant expression of the PUR protein and/or mutations in the PUR gene. The present sequence represents an oligomucleotide used in the identification and characterisation of the PUR protein and its sequence element PUR repeat, in an example from the
               Oligonucleotide MR0700 used in PUR identification/characterisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monoclonal antibody specific for PUR protein - useful for treating
                                                   PUR element; PUR-alpha; hyperproliferative disease; cancer; human; monoclonal antibody; identification; characterisation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromatin; DNA hybridization; DNA amplification; DNA microarray; diagnosis; ss; primer; PCR; OLIG2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.0%; Score 15.6; DB 2; Length 24; 50.0%; Pred. No. 4.8e+03; ive 7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3' primer for PCR of DNase I treated OLIG2 chromatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24 BP; 2 A; 14 C; 0 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                 SINAI SCHOOL MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 UNGUCUCUCUTUCGCCACCUC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; Col 27; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAY-2005; 2005WO-US019150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAY-2004; 2004US-0575478P.
                                                                                                                                                                                                                                                                                                       93US-00014943.
95US-00470911.
                                                                                                                                                                                                                                                  95US-00486809.
                                                                                                                                                                                                                                                                                       92US-00938189
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                                                                                                                                                                                                                                                                                                                                                                                                      Johnson EM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEE94315 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-152881/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2005118873-A2.
                                                                                                                                                                                                                                                                                                                                                                 TNUOM ( NUOM)
                                                                                                                                                                                                                                                                                                                                                                                                      Bergemann AD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-FEB-2006
                                                                                                                                                                                                                                                07-JUN-1995;
                                                                                                                                                                                                                                                                                       28-AUG-1992;
                                                                                                                                                                                                                                                                                                                             06-JUN-1995;
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                                                                                                                                                                        US5869622-A.
                                                                                                                                                                                                              09-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
                                                                                                                                                                                                                                                                                                         02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis;
                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEE94315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
AEE94315/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hyperproliferative diseases such as cancer. FUR antibodies may be used diagnostically to detect aberrant expression of the PUR protein and/or mutations in the PUR gene. The present sequence represents an oligonucleotide used in the identification and characterisation of the PUR protein and its sequence element PUR repeat, in an example from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a monoclonal antibody that specifically binds to an epitope of the PUR protein. Antibodies that bind to the PUR protein and neutralise PUR activity may be used to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                     Gaps
                                                                                                                                                                                                                                                                                                         Oligonucleotide MF0677 used in PUR identification/characterisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monoclonal antibody specific for PUR protein - useful for treating
                                                                                                                                                                                                                                                                                                                                               PUR element; PUR-alpha; hyperproliferative disease; cancer; human; monoclonal antibody; identification; characterisation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.0%; Score 15.6; DB 2; Length 24; 50.0%; Pred. No. 4.8e+03; ive 7; Mismatches 4; Indels.
Best Local Similarity 50.0%; Pred. No. 4.8e+03; Matches 11; Conservative 7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 24 BP; 8.A; 0 C; 14 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SINAI SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 UNGUCUCCUUUCGCCACCUC 24
                                                                                 2 TTTTCTCTCCCTCCACCTC 23
                                                         3 unguenecucientucecene 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 TTTTCTCCCTCCACCACCTC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example; Col 27; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                              BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-00486809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92US-00938189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93US-00014943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity 50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24
                                                                                                                                                                                              AAX04070 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Johnson EM;
                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX04075 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-152881/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNUOM ( NUOM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bergemann AD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-AUG-1992;
02-FEB-1993;
06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-1995;
                                                                                                                                                                                                                                                                     12-APR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5869622-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX04075;
                                                                                                                                                                                                                                  AAX04070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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RESULT 8 AAX04075

ઠ 요 HXXXH

Gaps

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Hall JG; V, Ma W; Takova TY;

Lyamichev

(THIR-) THIRD WAVE TECHNOLOGIES INC.

Allawi H,

11-JAN-2001; 2001US-00758282 24-MAY-2001; 2001US-00864426. 24-MAY-2001; 2001US-00864636.

24-MAY-2001; 2001WO-US017086 24-MAY-2000; 2000US-00577304

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determining the hybridization of a capture probe to a treated sample amplification products and the untreated sample amplification products and the untreated sample amplification products and the untreated sample amplification products. Specifically, the method comprises preparing a chromatin sample from cells, the chromatin sample comprising genomic DNA segments or genomic DNA with one or more open chromatin sites; treating a first portion of the chromatin sample with an open chromatin DNA cleaving agent to produce fragments; performing a first amplification reaction using the fragments as a substrate, to produce treated esample amplification products; performing a second amplification reaction using a second portion of the chromatin sample, where the second portion is not treated samplification of the chromatin DNA cleaving agent, to produce untreated-sample amplification products with a capture probe; and cherming the hybridization of the capture probe; and where reduced hybridization of the capture probe; and where reduced hybridization of the capture probe to the products of the capture probe to the untreated sample amplification products approbe to the untreated sample amplification products are checked sample amplification products and the capture probe to the untreated sample amplification of the capture probe to the untreated sample amplification products indicates the presence of open chromatin in the genomic DNA. Also given the capture probe to the untreated sample amplification group chromatin state profiling array, for detecting the presence of open chromatin in genomic DNA, used in the diagnostic and prognostic methods, and are useful for monitoring the presence of open chromatin in genomic DNA. The methods and chromatin at a companion of the untreated sample amplification products are useful for detecting open chromatin in genomic DNA, used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatment and evaluating the response of cells and patients to candidate or established therapeutic agents. The present sequence is a 3' reverse primer for one-sided PCR amplification of DNase I treated chromatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          new invention relates to detecting open chromatin in genomic DNA by
                                                                                                                                                                                                                                                                                                                                                                                             Detecting open chromatin comprises determining hybridization of or capture probe to the treated- and untreated-sample amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fragments, deposited on a chromatin profiling array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 37; 43pp; English.
                                                                                                                                                                                                                                                           WPI; 2006-047578/05.
(CEMI-) CEMINES INC.
                                                                                                                                                                                                                                                                                                                                                                               Detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              products.
                                                                                                                                 Neuman T;
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Gaps
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                                                                                                                          65.0%; Score 15.6; DB 15; Length 25; 40.9%; Pred. No. 4.8e+03;
                                                                                                                                Indels
                                                                                                                     Sequence 25 BP; 13 A; 0 C; 11 G; 1 T; 0 U; 0 Other;
                                                                                                                                9; Mismatches
                                                                                                                                Conservative
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AUJGUCUCUCCUUUCGCCACCU 23
                   22 ATTCTCTCTTTTTCTCCTCT 1
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ADI94591 standard; DNA; 21
      ADI94591:
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BP

(first entry) 04-NOV-2004

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Gaps

; 0

Indels

7; 24

DB 7; Length 21;

Murine IFN-gamma associated probe SEQ ID 2144.

functional domain; nucleic acid cleavage assay; detection; microorganism; RNA genome; hepatitis human immunodeficiency virus; ss; probe.

Mus musculus

WO200190337-A2

29-NOV-2001

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This invention describes a novel composition comprising an enzyme which contains a heterologous functional domain that provides altered to contains a heterologous functional domain that provides altered to comprise assay. The enzyme comprises a 5' nuclease, preferably a thermostable 5' nuclease, or a polymerase which is altered in sequence related to a naturally occurring sequence of a polymerase such that it exhibits reduced DNA synthetic activity from that confirmed polymerase is a conformation of the nuclear of thermostable polymerase from a Thermus species such as T. aquaticus, T. flaivus, T. filiformus or T. scotoductus. The enzyme comprises a heterologous functional domain, an amino acid sequence that provides an improved substrate binding activity in the nucleic acid cleavage assay and an amino acid sequence that provides improved background specificity in the nucleic acid cleavage structure comprises a RNA target nucleic acid (a cytochrome Cereavage structure comprises as RNA target nucleic acid (a cytochrome PSSO, or cytokine RNA). Cleavage product, which is then detected by detecting radioactivity luminescence, mass or fluorescence energy transfer or by detecting radioactivity luminescence, plosphorescence, fluorescence colarage. The enzyme is useful for cleavage asposing a sample (a cell lysate) comprising substrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid to the enzyme which produces at least one detectable cleavage product. The enzyme is employed for detecting target DNAs and RNAs comprising wild-type and mutant alleles of genes including genes from humans, other animal or lants that are or may be associated with disease or other conditions. In addition, the enzymes may be useful for
                                                                                                                                                                                                                                                                                                                                                 Composition comprising enzyme which comprises heterologous functional domain that provides altered functionality in nucleic acid cleavage assay, useful for cleaving nucleic acid, and detecting presence of RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detecting and identifying strains of microorganisms including bacteria, fungi, protozoa, ciliates and viruses, preferably detecting and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fungi, protozoa, ciliates and viruses, preferably detecting and identifying viruses having RNA genomes, such as hepatitis C and human
                                                                                                                                                                                Kaiser M, Kwiatkowski RW, Lukowiak AA, Lyamicher
nnoz MC, Olson SM, Schaefer JJ, Skrzypczynski Z,
L, Lyamichev NE, Neri BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21 BP; 9 A; 3 C; 8 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.3%; Score 15.2; DB 7
50.0%; Pred. No. 7e+03;
iive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine IFN-gamma associated probe SEQ ID 2142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 95; SEQ ID NO 2144; 1266pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:|:|:||:|| :|
Greteretringecagne 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GUCUCCUUUCGCCACCUC
                                                                                                                                                                                                            Ip HS, Kale...
Olson-Munoz MC, Olson...
'' KL, Lyamichev NE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADI94589 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 50.0°
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunodeficiency virus.
                                                                                                                                                                                                                                                                                                           WPI; 2002-083110/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADI94589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ហ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
                                                                                                                                                                                                                                                                                                                                                                                                                          target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADI94589/c
ID ADI94
XX
AC ADI94
XX
DT 04-NC
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nuclease; polymerase;
C;
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Composition comprising enzyme which comprises heterologous functional domain that provides altered functionality in nucleic acid cleavage assay, useful for cleaving nucleic acid, and detecting presence of RNA
        functional domain; nucleic acid cleavage assay; nuclease; polymerase;
detection; microorganism; RNA genome; hepatitis C;
human immunodeficiency virus; 85; probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 63.3%; Score 15.2; DB 7; Length 22; Best Local Similarity 50.0%; Pred. No. 7.1e+03; Matches 10; Conservative 7; Mismatches 3; Indels
                                                                                                                                                                                                                                      , Bartholomay CT, Chehak L, Curtis ML, Eis PS,
Kaiser M, Kwiatkowski RW, Lukowiak AA, Lyamichev
noz MC, Olson SM, Schaefer JJ, Skrzypczynski Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detecting and identifying strains of microorganisms flungi, protozoa, ciliates and virues, preferably de identifying virues having num
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22 BP; 9 A; 3 C; 9 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                   claim 95; SEQ ID NO 2142; 1266pp; English.
                                                                                                                                                                                                                 (THIR-) THIRD WAVE TECHNOLOGIES INC
                                                                                                                                                   24-MAY-2000; 2000US-00577304.
11-JAN-2001; 2001US-00758282.
24-MAY-2001; 2001US-00864426.
24-MAY-2001; 2001US-00864636.
                                                                                                                               24-MAY-2001; 2001WO-US017086.
                                                                                                                                                                                                                                                                                                  WPI; 2002-083110/11.
                                                                                                                                                                                                                                                    Ip HS, Kaiser olson-Munoz MC,
                                                                                 WO200190337-A2
                                                           Mus musculus.
                                                                                                         29-NOV-2001
                                                                                                                                                                                                                                                                           Vedvik KL,
                                                                                                                                                                                                                                         Allawi H,
                                                                                                                                                                                                                                                                                                                                                                target.
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Neri BP

Lyamichev NE,

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gene for a structural protein of cartilage comprising a sequence identified in Table I (Page 18-31). Table I includes 179 primer sequences (see AAQ65728-Q65906). The following details are given for primer 96: Region/exon: 31 Direction: sense Primer position: 12824 (Updated on 25-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and other diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             functional domain; nucleic acid cleavage assay; nuclease; polymerase; detection; microorganism; RNA genome; hepatitis C; human immunodeficiency virus; ss; probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 18 claims primers for use in detecting mutations in a mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting genetic pre-disposition to osteoarthritis - and other disk involving mutation in cartilage protein genes, by amplification and analysis of DNA and comparison with standards.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baldwin C;
                                                                                                                                                                                                                                             Type II procollagen, COL2Al; amplification, primer; polymerase chain reaction; PCR; osteoarthritis; cartilage; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ala-Kokko L, Williams CJ, Ritvaniemi P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18 BP; 1 A; 10 C; 1 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 14.4; DB 2;
Pred. No. 1.5e+04;
5; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine IFN-gamma associated probe SEQ ID 2146.
                                                                                                                                                                                                     Type II procollagen sequencing primer 96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 18; Page 26; 112pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYJE-) UNIV JEFFERSON THOMAS
                                           ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60.0%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 CTCCTTCCCCACCTC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93WO-US010964.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92US-00977284.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADI94593 standard; DNA; 20
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                                           AAQ65826 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 CUCCUUUCGCCACCUC
                                                                                                                                      (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 62.5
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ahmad NN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1994-183530/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prockop DJ,
Hopkinson I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                     WO9411532-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAY-1994.
                                                                                                                                    25-MAR-2003
20-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADI94593;
                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                        AAQ65826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADI94593
                     AAQ65826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel composition comprising an enzyme which contains a hererologous functional domain that provides altered contains a hererologous functional domain that provides altered contains a hererologous functional domain that provides altered in containality in a nucleic acid cleaves easey. The enzyme comprises a 5' conclease, preferably a thermostable 5' nuclease, or a polymerase which is altered in sequence related to a naturally occurring sequence of a polymerase such that it exhibits reduced DNA synthetic activity from that of thermostable polymerase from a Thermus species such as T. aquaticus, T. flavus, T. thermophilus, T. filiformus or T. scotoductus. The enzyme comprises a heterologous functional domain, an amino acid sequence that provides an improved substrate binding activity in the nucleic acid cleavage sasay and an amino acid sequence that provides improved cleavage structure comprises a RNA target mucleic acid (a cytochrome Cleavage structure comprises a RNA target mucleic acid (a cytochrome Cleavage structure comprises a RNA target mucleic acid (a cytochrome Cleavage structure comprises a RNA target mucleic acid (a cytochrome CC qenerates an non-target cleavage product, which is then detected by detecting radioactivity luminescence, phosphorescence, fluorescence CC which involves exposing a sample (a cell lysate) comprising substrate cucleic acid to the enzyme is employed for detecting target DNAs and cleavage product. The enzyme is employed for detecting cleavage product. The enzyme is employed for detecting farget DNAs and cleavage product. The enzyme is employed for detecting farget DNAs and cleavage product. The enzyme is employed for detecting farget DNAs and disease or other animal or plants that are or may be associated with disease or other conditions. In addition, the enzyme is remptored.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                      Hall JG;
V, Ma W;
Takova TY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               orotozoa, ciliates and viruses, preferably detecting and
ing viruses having RNA genomes, such as hepatitis C and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Gaps

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enzyme; plant; a mays; radish;

potato; Solanum tuberosum; rice; Oryza sativa; maize; Zea mays; radis! Raphanus sativus; Flaveria brownii; primer; expression vector; probe; Agrobacterium tumefaciens; sugar; storage; temperature; ss.

ATP-dependent fructose-6-phosphate 1-phosphotransferase

S.tuberosum PFK probe PFK23

(revised)
(first entry)

25-MAR-2003 12-OCT-1995

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This invention describes a novel composition comprising an enzyme which contains a heterologous functional domain that provides altered contains a heterologous functional domain that provides altered contains in a nucleic acid cleavage assay. The enzyme comprises a 5' muclease, preferably a thermostable 5' muclease, or a polymerase which is altered in sequence related to a naturally occurring sequence of a colymerase such that it exhibits reduced DNA synthetic activity from that of the naturally occurring polymerase. Preferably the polymerase is a chermostable polymerase from a Thermus species such as T. aquaticus, T. Clavus, T. thermophilus, T. filiformus or T. scotoductus. The enzyme comprises a heterologous functional domain, an amino acid sequence that provides an improved substrate binding activity in the nucleic acid (a cytochrome package assay and an amino acid sequence that provides improved cleavage structure comprises a RNA target nucleic acid (a cytochrome P450, or cytokine RNA). Cleavage product, which is then detected by detecting radioactivity luminescence, phosphorescence, fluorescence comprisation or charge. The enzyme is useful for cleavage structure comprises. The enzyme is useful for cleavaing a nucleic acid cother enzyme which produces at least one detectable cleavage product. The enzyme is employed for detecting target DNAs and RNAs comprising wild-type and mutant alleles of genes including genes from humans, other animal or plants that are or may be associated with disease or other conditions. In addition, the enzyme any beatsymes and beatsymes and any plants any plants and any plants any plants and any plants any p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detecting and identifying strains of microorganisms including bacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition comprising enzyme which comprises heterologous functional domain that provides altered functionality in nucleic acid cleavage assay, useful for cleaving nucleic acid, and detecting presence of RNA
                                                                                                                                                                                                                                                                                                                                                      Hall JG;
V, Ma W;
Takova TY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preferably detecting and such as hepatitis C and human
                                                                                                                                                                                                                                                                                                                                                 Allawi H, Bartholomay CT, Chehak L, Curtis ML, Bis PS, Ip HS, Kaiser M, Kwiatkowski RW, Lukowiak AA, Lyamichev Olson-Munoz MC, Olson SM, Schaefer JJ, Skrzypczynski Z, Vedvik KL, Lyamichev NB, Neri BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fungi, protozoa, ciliates and viruses, preferably
identifying viruses having RNA genomes, such as h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 9 A; 3 C; 7 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 95; SEQ ID NO 2146; 1266pp; English
                                                                                                                                                                                                                                                                                                 (THIR-) THIRD WAVE TECHNOLOGIES INC
                                                                                                                                                          2000US-00577304
2001US-00758282
2001US-00864426
                                                                                                       24-MAY-2001; 2001WO-US017086
                                                                                                                                                                                                                                              24-MAY-2001; 2001US-00864636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-083110/11
                                                                                                                                                                                      11-JAN-2001;
24-MAY-2001;
                                                                                                                                                             24-MAY-2000;
                                                     29-NOV-2001.
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of plant

DNA coding for fructose-6-phosphate 1-phosphotransferase - of pla origin, for prodn. of transformant plant cells with altered sugar

Sxample 7; Page 15; 79pp; Japanese.

content

Tyson HR,

Kasaoka K,

Mine T,

Hiyoshi T,

WPI; 1995-098757/13.

(NISB) JAPAN TOBACCO INC

94WO-JP001352 93JP-00226454

16-AUG-1994; 19-AUG-1993;

WO9505457-A1

Synthetic.

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encoding an N-terminal peptide (AAR71610) from the novel potato (Solanum tuberosum) ATP-dependent fructose-6-phosphate 1-phosphotransferase enzyme (BC 2.7.1.11; PFK). The probe was used to obtain 11 clones of the PFK gene. These clones, amplified by PCR using the primers (AAQ85990-3), ligated into the plasmid pBluescript SKII(-). The full length gene (AAQ85982) was used to generate the expression vector pPFK(35S) which was transformed into plants via Agrobacterium tumefaciens. Transformed plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expressing the enzyme can be used to produce varieties that have alrered sugar content on storage at low temperatures. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                          from a 60 bp amplified fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA-targeting conjugate, anticancer drug; viral DNA-cleaving agent; viral DNA-binding agent; solid support; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.0%; Score 14.4; DB 2; Length 23; 56.2%; Pred. No. 1.6e+04; Live 6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23 BP; 9 A; 0 C; 9 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                          sequence of the probe PFK23 derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV-1 proviral DNA fragment 29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX56946 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTCCTTTCACCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 56.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sugar content on s
correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX56946/
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1; Indels

Mismatches

Local Similarity 56.2 es 9; Conservative

Best Loca Matches

Query Match

20

19 GICTCTCCTTTTGCCA 5 GUCUCUCCUUUCGCCA

BP.

AAQ85989 standard; DNA; 23

RESULT 14 AAQ85989/ ID AAQ8 XX AC AAQ8

AAQ85989

ö

Gaps

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(SLOK ) SLOAN KETTERING INST CANCER RES. (ZWBI-) ZW BIOMEDICAL RES AG.
      12-MAY-1995;
                       Watanabe KA,
           13-MAY-1994;
  23-NOV-1995
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Ren W,

95WO-US006379 94US-00242664

Derivatised solid supports and reagents for oligo:nucleotide synthesis - and new oligo:nucleotide phosphoramidate conjugates. WPI; 1996-010846/01

This invention describes novel derivatised solid supports of formula S'-L-Z-CH2CH2-R, where: S' = a solid support; L = a bond or an (in) organic linker; Z = SO2 or S-S; R = OH, an H-phosphonate, alkanephosphonate, phosphotriester, phosphite triester, phosphoramidate or phosphoramidate group, or an optionally substituted or modified nucleotide (N'), or an oligonucleotide of formula (N')R2; g = 1-200; R1 = a protecting group; R2 = an H-phosphonate, phosphorate, phosphite triester, phosphite triester, phosphite diester, phosphoramidate or phosphoramidite group, OH, OR1, SR1 or Disclosure; Page 48; 68pp; English

phosphoramidate or phosphoramidite group, OH, OR1, SR1 or
CCC CPCH2CH2ZCH2CH2CR1. Also mentioned are compounds of formula
CCC CPCH2CH2ZCH2CH2CR2CR1. Also mentioned are compounds of formula
CCC R3GH2GH2ZCH2CH2CH2R4, where: R3 = a protecting group; and R4 = OH or an HCCC Phosphorate, alkanephosphorate, phosphoriester, phosphite triester,
CCC phosphoramidite group. Also claimed are new phosphoramidates, a
CCC process for preparing an oligonucleotide 5'-phosphate, a process for
CCC proparing a solid support useful for preparation of an oligonucleotide 3'
CCC phosphate, a process for preparing an oligonucleotide 3'-phosphate and a
CCC process for preparing an oligonucleotide 3'-phosphate and a
CCC process for preparing an oligonucleotide 3'-phosphate and a
CCC process for preparing an oligonucleotide 3'-phosphate and
CCC oligonucleotide 3'- and/or 5'-phosphates may be used to prepare DNACLASCHING OR - binding agents. The process for preparing oligonucleotide
CCC cleaving or -binding agents. The process for preparing oligonucleotide
CCC 3',5'-diphosphates is a simple and suitable for use in automatic DNA
CSC 3',5'-diphosphates is a simple and suitable for use in automatic DNA
CSC 3',5'-diphosphates is a simple and suitable for use in automatic DNA
CSC 3',5'-diphosphates is a simple and suitable for use in automatic DNA
CSC 3',5'-diphosphates is a simple and suitable for use in automatic DNA
CSC 3',5'-diphosphates is a simple and suitable for use in automatic DNA
CSC 3',5'-diphosphates is a simple and suitable for use in automatic DNA
CSC 3',5'-diphosphates is a simple and suitable for use in automatic DNA
CSC 3',5'-diphosphates by a sequence represents a fragment of the HIV-1 provins
CSC 303 to standardise OS field)

Sequence 21 BP; 13 A; 0 C; 7 G; 1 T; 0 U; 0 Other;

Gaps ö Query Match 59.2%; Score 14.2; DB 2; Length 21; Best Local Similarity 36.8%; Pred. No. 1.9e+04; Matches 7; Conservative 9; Mismatches 3; Indels

1 UAUUGUCUCCCUUUCGCC 19

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19 TTTATCTCTCCTTTCTCC 1

Search completed: June 19, 2007, 13:01:32 Job time : 248.5 secs

C 25 13.8 57.5 C 26 13.6 56.7 C 26 13.6 56.7 C 27 13.6 56.7 C 29 13.4 55.8 C 31 13.4 55.8 C 33 13.4 55.8 C 33 13.4 55.8	ннннн	13.4 55. 13.4 55. 13.2 55. 13.2 55.	RESULT 1	US-US-104-945-94-94C Sequence 3, Applicat RENERAL INFORMATION APPLICANT: Berge TITLE OF INVENTION NUMBER OF SEQUENC CORRESPED: Pen ADDRESSE: Pen STREET: 1155 A STREET: New York CONTRESS New YORK STREET: NEW YORK STRE	COUNTRY: U.S.A. 1 ZIP: 10036-271 COMPUTER READABLE: COMPUTER: F COMPUTER: IBM COMPUTER: IBM COMPUTER: IBM SOFTWARE: PATER CURRENT APPLICATION	## APPLICATION NUM	z ·· ˈˈˈˈˈˈˈˈˈˈˈˈˈˈˈˈˈˈˈˈˈˈˈˈˈˈˈˈˈˈˈˈˈˈ
GenCore version 6.2.1 Copyright (c) 1993 - 2007 Biocceleration Ltd. OM nucleic - nucleic search, using sw model Run on: June 19, 2007, 12:53:27 ; Search time 256 Seconds (without alignments) 175.760 Million cell updates/sec	Title: US-10-604-726A-5136 Perfect score: 24 Sequence: 1 uauugucucuucgccaccuc 24 Scoring table: IDENTITY_NUC Gapop 10-0 , Gapext 1.0	Searched: 1403666 seqs, 935554401 residues Total number of hits satisfying chosen parameters: 960512 Minimum DB seq length: 0 Maximum DB seq length: 25	ocessing: Minimu Maximu Listir	Isbued Patents NA:* 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB. 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB. 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6_COMB. 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6_COMB. 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB. 6: /EMC_Celerra_SIDS3/ptodata/2/ina/PCOMB. 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCOMB. 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PCOMB. 9: /EMC_Celerra_SIDS3/ptodata/2/ina/PCOMB. 10: /EMC_Celerra_SIDS3/ptodata/2/ina/PCOMB. 10: /EMC_Celerra_SIDS3/ptodata/2/ina/ABCCOMB.	Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES Result No. Score Match Length DB ID Predicted by charch length DB ID	15.6 65.0 24 2 US-08-014-943A-3 Sequence 15.6 65.0 24 2 US-08-014-943A-15 Sequence 15.6 65.0 24 2 US-08-048-421-20 Sequence 15.6 65.0 24 2 US-08-486-421-38 Sequence 15.6 65.0 24 2 US-08-486-421-38 Sequence 15.6 65.0 24 2 US-08-486-809-20 Sequence 15.6 65.0 24 2 US-08-486-809-20 Sequence 15.6 65.0 24 2 US-08-486-809-38 Sequence 14.4 60.0 18 2 US-07-977-284A-99 Sequence 14.4 60.0 18 2 US-07-977-284A-99 Sequence	4.2 59.2 21 2 US-08-242-664-38 Sequence 38, 4.2 59.2 21 2 US-08-448-138-38 Sequence 38, 4.2 59.2 21 2 US-08-448-138-38 Sequence 38, 4.2 59.2 21 2 US-08-649138-38 Sequence 38, 4.2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2

Appl	Appl	A , 61	:71,	App		Appl	App		7, A	8, A	٥, ٩	49,	Appl	App							
10,	10,	6439	119671,	100,	100,	26,	57,	56,	57,	26,	57,	56,	57,	365,		14417,	14428	5743	117149	15,	322,
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
US-09-506-852-10	US-10-392-706-10	US-09-396-196G-64399	US-09-396-196G-119671	US-07-977-284A-100	US-08-256-426B-100	US-08-445-463B-56	US-08-445-463B-57	US-08-445-464C-56	US-08-445-464C-57	US-08-044-857D-56	US-08-044-857D-57	PCT-US94-03437-56	PCT-US94-03437-57	US-09-544-398B-365	US-09-543-771B-365	US-09-396-196G-14417	US-09-396-196G-14428	US-09-396-196G-57430	US-09-396-196G-117149	US-09-265-630-15	US-08-983-605-322
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20	20	25	25	17	17	24	24	24	24	24	24	24	24	25	25	25	25	25	25	20	21
57.5	57.5	56.7	56.7	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.0	55.0
13.8	13.8	13.6	13.6	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.2	13.2
24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

Of PUR Protein	B 2; Length 24; +02; 4; Indels 0; Gaps
RESULT 1 US-08-014-943A-3/C Sequence 3, Application US/08014943A Patent No. 554551 GENERAL INFORMATION: APPLICANT: Johnson, Edward M. APPLICANT: Bergemann, Andrew D. TITLE OF INVENTION: Cloning And Expression Of NUMBER OF SEQUENCES: 26 COUNTRY: US. A. STREET: 1155 Avenue of the Americas CITY: New York STRATE: New York COUNTRY: U.S. A. ZIP: 10036-0711 COMPUTER: IPP PC COMPatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Petentin Release #1.0, Version #1 CUMPUTER: IPP PC COMPatible OPERATING SYSTEM: O2/FEB1992 CLASSIFICATION NUMBER: US/08/014,943A FILING DATE: 02/FEB1992 CLASSIFICATION NUMBER: 90.742 REGISTRATION NUMBER: 30,742 REGISTRATION NUMBER: 30,742 REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 6923-033 TELEPRONE CHARACTERISTICS: LENGTH: 24 base pairs TTELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 24 base pairs TTPE: MOLECULE TYPE: UNKNOWN WOLFCULE TYPE: DNA (Genomic) US-08-014-943A-3:	Query Match 65.0%; Score 15.6; DB 2 Best Local Similarity 50.0%; Pred. No. 6.46+02 Matches 11; Conservative 7; Mismatches

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Sequence 38, Application US/08486421
Sequence 38, Application US/08486421
Sequence 10. 5672479
GENERAL INFORMATION:
APPLICANT: Johnson, Edward M.
APPLICANT: Bergemann, Andrew D.
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 24;
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COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,421
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION 435
PRIOR APPLICATION NUMBER: US/08/486,421
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT ARPLICATION DATA:
APPLICATION NUMBER: US/08/486,421
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/470,911
APPLICATION NUMBER: US/08/470,911
FILING DATE: 06-JUN-1995
ATTONINY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.0%; Score 15.6; DB 2; 50.0%; Pred. No. 6.4e+02;
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STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923-053
FELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923-053
TELECOMMUNICATION INFORMATION:
                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 unguenceconnegeeacene 24
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: (212) 869-9741/8864
66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 24 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS
MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Johnson, Edward M.
APPLICANT: Bergemann, Andrew D.
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                        Sequence 15, Application US/08014943A
Patent No. 554551
GENERAL INFORMATION:
APPLICANT: Bergemann, Edward M.
APPLICANT: Bergemann, Andrew D.
TITLE OF INVENTION: Cloning And Expression Of PUR Protein
CORRESPONDENCE 3.
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
BLILOATION NUMBER: US/08/014,943A
FILING DATE: 02)FEB)1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.0%; Score 15.6; 50.0%; Pred. No. 6.
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STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: C. ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"MEDIUM TYPE: Flopp
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Patent No. 5672479
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 02) FEB) 1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COFUZEL, LAUEA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212,790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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US-08-014-943A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 24 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10036-2711
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
.....hes 11; Conserva
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STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New Yor!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                         RESULT 2
US-08-014-943A-15
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                    Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Johnson, Edward M.
APPLICANT: Johnson, Andrew D.
APPLICANT: Bergemann, Andrew D.
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                            Query Match 65.0%; Score 15.6; DB 2; Best Local Similarity 50.0%; Pred. No. 6.4e+02; Matches 11; Conservative 7; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.0%; Score 15.6; DB 2; 50.0%; Pred. No. 6.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 UNGUCUCCUUNUCGCCACCUC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20, Application US/08470911
Patent No. 5756684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 TTTTĊTĊCTCCAĊCAĊCTC 2
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10S-08-470-911-38
'Sequence 38, Application US/08470911
'Patent No. 5756684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
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                                    SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTER.FSTICS:
LENGTH: 24 base pairs
                                                                         LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                TOPOLOGY: linear;
MOLECULE TYPE: DNA
US-08-486-421-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New York COUNTRY: U.S.A.
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US-08-470-911-20/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-470-911-20
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Sequence 20, Application US/08486809

Sequence 20, Application US/08486809

Sequence 20, Application US/08486809

GENERAL INFORMATION:
APPLICANT: Bergemann, Andrew D.
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREBT: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 24;
APPLICANT: Johnson, Edward M.
APPLICANT: Bergemann, Andrew D.
TILLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,911
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SUPERATION NUMBER: US/08/486,809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 15.6; DB 2;
Pred. No. 6.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Mismatches
                                                                                                      ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                         STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 UNGUCUCUCCUTUCGCCACCUC 24
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2 TTTTCTCCTCCACCACCTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/ACENT INPOGRATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923
TELECOMMUNICATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 65.0%;
Best Local Similarity 50.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 24 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 07-JUN-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA
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: U.S.A.
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COUNTRY: U.S.A.
ZIP: 10036-2711
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Length 24;

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65.0%; Score 15.6; DB 2; ilarity 50.0%; Pred. No. 6.4e+02; Conservative 7; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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LENGTH: 18
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
FILING DATE: 13-NOV
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: NUCLEIC ACID
STRANDEDNESS: SINGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: LINEAR
; ANTI-SENSE: NO
US-07-977-284A-99
    Query Match
Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
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                                                                                                                                                                                                                                                                                                                                                                            65.0%; Score 15.6; DB 2; Length 24; 50.0%; Pred. No. 6.4e+02; tive 7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 38, Application US/08486809
Patent No. 5865622
GENERAL INFORMATION:
APPLICANT: Johnson, Edward M.
APPLICANT: Bergemenn, Andrew D.
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,809
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-0000
TELEPAX: (210)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,911
FILING DATE: 06-UUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LABIRA A.
                                                                NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
          US 08/470,911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 UNGUCUCCUTUCGCCACCUC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 TTTTCTCTCCTCCACCTC 2
                                                                                                                                                            TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic) US-08-486-809-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
                            FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 50.09
Matches 11; Conservative
                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE:
US-08-486-809-38
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Gaps
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STREET: One Liberty Place, 46th floor
CITY: Philadelphia
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                                                                                                                                                                                                                                                                                                                      APPLICANT: Williams, Charlene J.
APPLICANT: Ritvaniemi, Pertti
APPLICANT: Baldwin, Clinton
APPLICANT: Hopkinson, Ian
APPLICANT: Ahmad, Nilofer Nina
APPLICANT: Ahmad, Nilofer Nina
TITLE OF INVENTION: PREDISFOSITION FOR OSTEOARTHRITIS
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

60.0%; Score 14.4; DB 2;
Best Local Similarity 62.5%; Pred. No. 2.1e+03;
Matches 10; Conservative 5; Mismatches 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ыж: US/07/977,284A
13-NOV-1992
NN: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
US-08-256-426B-99
Sequence 99, Application US/08256426B
Patent No. 5948611
GENERAL INFORMATION:
                                                                                                                                                                                                      Sequence 99, Application US/07977284A
Patent No. 5558988
                                             3 UNGUCUCUCCUUUCGCCACCUC 24
                                                                                                                                                                                                                                                                           Prockop, Darwin J.
Ala-Kokko, Leena
Williams, Charlene J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: DeLuca, Mark
REGISTRATION UNDRER: 33,229
REFRENCE/DOCKET UNDRER: TUU-
TELECOMMUNICATION INFORMATION:
TELEPAR: (215) 568-3100
TELEPAR: (215) 568-3100
INFORMATION FOR SEQ ID NO: 99:
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us-10-604-726a-5136.sizlim25.rni

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Query Match 59.2%; Score 14.2; DB 2; Length 21; Best Local Similarity 36.8%; Pred. No. 2.7e+03; Matches 7; Conservative 9; Mismatches 3; Indels
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sequence 38, Application US/08484138
sequence 38, Application US/08484138
sequence 38, Application US. 563250
sequence 38, Application:
APPLICANT: Watanabe, Kyoichi A.
APPLICANT: Wail, Red, Wu-Yun
APPLICANT: Wail, Reger
TITLE OF INVENTION: Complementary DNA and Toxins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
COUNTRY: U. S.A.
ZIP: 10036
COMPUTER: READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44Mb
COMPUTER: IBM PC
OPREMATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,138
FILING DATE: June 7, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION NUMBER: 28,678
TELECOMMUNICATION NUMBER: 212-977-9550
TELEEPAX: 212-664-0525
TUNDARTAN AND CON TOWN CON TOWN
THE AND CON CONT TOWN
THE CONTROL OF TOWN
THE CONTROL O
                   MEDIUM TYPE: 3.5 inch 1.44Mb
COMPUTER: 1BM PC compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,664
FILING DATE: May 12, 1994
CLASSIFICATION: B.14
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44683
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-97-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 UAUUGUCUCCUUUCGCC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 38: SEQUENCE CHARACTERISTICS: LENGTH: 21 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: DNA (genomic) US-08-242-664-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-484-138-38/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5948611ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 60.0%; Score 14.4; DB 2; Length 18; Best Local Similarity 62.5%; Pred. No. 2.1e+03; Matches 10; Conservative 5; Mismatches 1; Indels
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Fatent No. 5571937
GENERAL INFORMATION:
APPLICANT: Watanabe, Kyoichi A.
APPLICANT: Ren, Wu-Yun
APPLICANT: Ren, Wu-Yun
TITLE OF INVENTION:
CORRESPONDENCES: 43
CORRESPONDENCES: 43
CORRESPONDENCES: Cooper & Dunham
STREET: 30 Rockefeller Plaza
                                                                                                                                                        APPLICANT: Hopkinson, Ian
APPLICANT: Ahmad, Nilofer Nina
TITLE OF INVENTION: Methods of Detecting A Genetic
NUMBER OF SEQUENCES: 293
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRX: USA.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,426B
FILING DATE: 03-FEB-1995
CLASSIFICATION TATE:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/977,284
FILING DATE: 12-NOV-1993
PRIOR APPLICATION NUMBER: US 07/977,284
FILING DATE: 13-NOV-1992
ATFORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: TJU-1082
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
                                                                                            Ritvaniemi, Pertti
Baldwin, Clinton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 CUCCUUUCGCCACCUC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 18
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: LINEAR; ANTI-SENSE: NO US-08-256-4268-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-08-242-664-38/c
                                                                                                                                                                                                                                                                                                                                                                              CITY: Phi
STATE: PA
COUNTRY:
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                                                                                            APPLICANT:
APPLICANT:
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1155 Avenue of the Americas
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STATE:
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                                                                                    Gaps
                                                     Length 21;
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APPLICANT: Bergemann, Andrew D.
TITLE OF INVENTION: Cloning And Expression Of PUR Protein
                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                            Complementary DNA and Toxins
                                                   Score 14.2; DB 2;
Pred. No. 2.7e+03;
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                                                                                    9; Mismatches
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Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                             E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US95/06379
FILING DATE: May 13, 1994
CLASSIFICATION:
                                                                                                                                                                                                                         PCT-US95-06379-38/c
; Sequence 38, Application PC/TUS9506379
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-014-943A-12/c
; Sequence 12, Application US/08014943A
Patent No. 5545551
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         APPLICANT: Watanabe, Kyoichi A. APPLICANT: Ren, Wu-Yun APPLICANT: Weil, Roger TITLE OF INVENTION: Complementary NUMBER OF SEQUENCES: 43 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: 3.5 inch 1.44Mb IBM PC
                                                                                                                      1 UAUTGUCUCUCCUTUCGCC 19
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.2%;
   DNA (genomic)
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                                                   59.2%;
36.8%;
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                                     Query Match
Best Local Similarity 36.5-
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
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: New York
RY: U.S.A.
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   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US95-06379-38
        ; MOLECOME 118
US-08-484-138-38
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GENERAL INFORMATION:
APPLICANT: Johnson, Edward M.
APPLICANT: Bergemann, Andrew D.
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                         PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 14; DB 2;
Pred. No. 3.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Mismatches
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/014,943A
FILING DATE: 02)FEB)1992
CLASSIFICATION: 435
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APPLICATION NUMBER: US 08/470,911
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,421
FILING DATE: 07-UUN-1995
                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 UNGUCUCUCCUUUCGCCACCUC 24
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Patent No. 5672479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFRENCE/DOCKET NUMBER: 6923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRA.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
AMBIUM TYPE: FLOPPY disk
COMPATIBLE

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 40.97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
                                                                             ZIP: 10036-2711
COMPUTER READABLE FORM
MEDIUM TYPE: Floppy
New York
: U.S.A.
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: U.S.A.
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CLASSIFICATION:
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Search completed: June 19, 2007, 13:10:06 Job time: 255.5 secs

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Sequence 2144, Ap Sequence 2144, Ap Sequence 2142, Ap Sequence 2142, Ap Sequence 2142, Ap Sequence 661177, Sequence 42396, A Sequence 42396, A Sequence 42396, A Sequence 43354, A

Sequence 67315, A Sequence 144888, Sequence 550631, Sequence 685018,

Sequence 217334, Sequence 720298, Sequence 538357, Sequence 276882,

Sequence

Sequence 116930, Sequence 949541, Sequence 426363, Sequence 67315, A

88872, F 47765, F 524825,

Sequence Sequence Sequence Sequence

Perfect score:

Sequence:

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Minimum DB E Maximum DB E

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APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
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TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-933-982-217334
US-11-036-317-720298
US-11-121-849-233357
US-11-136-527-276882
US-10-310-914A-1070230
US-09-864-636A-2144

US-09-864-426A-2144

US-00-884-636A-2142

US-09-864-636A-2142

US-09-864-636A-2142

US-10-084-839-2142

US-11-083-784-661177

US-11-081-244-661177

US-11-081-244-661177

US-11-0956-157-42396

US-10-956-157-42396

US-10-956-157-43354

US-10-956-157-43359

US-10-956-157-43859

US-10-910-914A-949541

US-10-310-914A-67315

US-10-310-914A-553631
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Pred. No. 3.7e+03;
7; Mismatches 3;
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SOFTWARE: PatentIn version 3.2
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Best Local Similarity
Matches 11; Conserv
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                                           US-10-719-900-980988
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LENGTH: 25
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1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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Sequence 21634, 1
Sequence 21637, 1
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Sequence 980988,
                                                                                                                                                                                                                                  June 19, 2007, 13:01:01 ; Search time 1262 Seconds (without alignments) 233.679 Million cell updates/sec
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                                       GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd.
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US-10-956-157-42579

US-10-956-157-88871

US-11-060-756-4774

US-11-310-914A-205339

US-11-136-527-276978

US-11-136-527-276978

US-11-136-527-276978

US-11-136-527-276978

US-11-036-317-35846

US-10-956-157-21624

US-10-956-157-21634

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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Match Length DB
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length: 25
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APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITS AND HUMAN PROFEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT APPLICATION NUMBER: US/10/956,157
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 88877
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APPLICANT: Wounts, William Martin
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT APPLICATION DOS: 303284
NUMBER OF SEQ ID NOS: 303284
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Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
Target Genes
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4.5e+03;
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Pred. No.
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Pred. No.
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Sequence 47788 Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
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Publication No. US20050118625A1
GENERAL INFORMATION:
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Best Local Similarity 45...
Local 11; Conservative
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Best Local Similarity 45.8
Matches 11; Conservative
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APPLICANT: Mounts, V
TITLE OF INVENTION: I
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; ORGANISM: probe
US-11-060-756-47774
                                                                                                                                          US-10-956-157-88877
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APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANT: Wounts, William
TITLE OF INVENTION: UNCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 88871
LENGTH: 25
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APPLICANT: Wounts, William
APPLICANT: Wounts, William
TITLB OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REPERENCE: 031986-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US,10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 42579
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Pred. No. 4.5e+03;
8; Mismatches 5; Indels
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                   CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 980988
LENGTH: 25
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. 4.5e+03;
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                                                                                                                                                                                                                                             66.7%; Score 16; DB 37.5%; Pred. No. 4.5e ive 10; Mismatches
CURRENT APPLICATION NUMBER: US/10/719,900
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 42579, Application US/10956157 Publication No. US20050118625A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       1 TTTTGTCTCTTTTTCTCCAGGTC 24
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Publication No. US20050118625A1
GENERAL INFORMATION:
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45.8%;
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Best Local Similarity 37.54
Matches 9; Conservative
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Best Local Similarity 45.8
Matches 11; Conservative
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Best Local Similarity 45.8
Matches 11; Conservative
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ORGANISM: Probe Sequence
US-10-956-157-88871
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; ORGANISM: Probe Sequence
US-10-956-157-42579
                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-980988
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US-10-956-157-42579/c
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APPLICANT: Wounts, William M
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-04100 (AM.01086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT APPLICATION NUMBER: US 60/574,294
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR PLING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 276903
LENGTH: 25
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Sequence 678730, Application US/10719900

Sequence 678730, Application US/10719900

Publication No. US20550026164A1

GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

FILE REFERENCE: 3528.1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT APPLICATION NUMBER: 06/427,808

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR PILING DATE: 2002 11 20

NUMBER OF SEQ ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 678730

LENGTH: 25
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Pred. No. 5.5e+03;
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Pred. No. 6.7e+03;
8; Mismatches 4;
    Pred. No. 5.5e+03;
8; Mismatches 2
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                                                                                                                                                                                                                     Sequence 276903, Application US/11136527 Publication No. US20050287570A1 GENERAL INFORMATION:
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    47.48;
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Best Local Similarity 47.4%;
Matches 9; Conservative
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Best Local Similarity 45.5%;
Matches 10; Conservative
  Best Local Similarity 47.4
Matches 9; Conservative
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ORGANISM: Mus musculus
US-10-719-900-678730
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Publication No. US2066003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: Uses thereof
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402.
SOFTWARE: Patentin version 3.3
SEQ ID NO 205339
LENGTH: 24
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Publication No. US20050287570A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wounts, William M

TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

CURRENT APPLICATION (MMDER: US/11/136,527

CURRENT FILING DATE: 2005-05-25

PRIOR APPLICATION NUMBER: US 60/574,294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15.8; DB 11; Length 24; Pred. No. 5.5e+03; 0; Mismatches 2; Indels C
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Pred. No. 4.5e+03;
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FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 302284
SOFTWARE: PATENTIN VERSION 3.2
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Best Local Similarity 89.5%;
Matches 17; Conservative
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 276878
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Best Local Similarity
Matches 11; Conserva
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                                                                                                                                                         ; TYPE: DNA
; ORGANISM: probe
US-11-060-756-47788
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                                                                                                             SEQ ID NO 47788
LENGTH: 25
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Search completed: June 19, 2007, 16:27:50 Job time : 1264 secs
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SOFTWARE: Patentin version 3.2
SEQ ID NO 21630
LENGTH: 25
                                    Query Match
Best Local Similarity 47.1%;
Matches 8; Conservative
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Best Local Similarity 47.1%;
Matches 8; Conservative
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US-10-956-157-21624
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Sequence 21624, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wounts, William

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

FILE REPERENCE: 03189-04300 (AM 101081)

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT FILING DATE: 2004-10-04
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Squence 498782, Application US/10310914A

Squence 498782, Application US/10310914A

Squence 498782, Application No. US20060003322A1

GRNERAL INFORMATION:
Shiler, Kvuzat

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Uses thereof

FILE REFERENCE: 06087.0200.CPUSO1

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT PILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3.3
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                                      APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REPERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR PPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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Pręd. No. 6.7e+03;
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Pred. No. 8
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94.1%;
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SOFTWARE: PatentIn version 3.2
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Best Local Similarity 94.1
Matches 16; Conservative
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Best Local Similarity 40.9
Matches 9; Conservative
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ORGANISM: Probe Sequence
                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-35846
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ORGANISM: Human
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LENGTH: 20
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LENGTH: 25
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LENGTH: 25
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APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REPERENCE: 031896-043000 (AM 101081)
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Length 25;
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Pred. No. 8.2e+03;
8; Mismatches 1;
DB 10;
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CURRENT FILING DATE: 2004-10-04
                                                                                                                                                                                                                                              Sequence 21630, Application US/10956157 Publication No. US20050118625A1 GENERAL INFORMATION:
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Sequence 860087, Sequence 1236716, Sequence 25290, A Sequence 151397, Sequence 151397, Sequence 247872, Sequence 247872,

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Score

Result Š

Sequence Sequence

Sequence Sequence

Sequence 1236716, Sequence 792768, Sequence 843298, Sequence 860087,

Perfect score:

Sequence:

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Scoring table:

Database

Sequence

Sequence 1245669, Sequence 1245759, Sequence 2484540, Sequence 792768, Sequence 843298,

Sequence 1077569,

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DETECTING GENE EXPRESSION IN ANIMAL
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0 US-10-714-333A-1245759
7 US-11-093-832-1077569
7 US-11-093-832-1245759
7 US-11-093-832-1245759
US-10-093-832-1245759
US-10-709-691B-43800
0 US-10-709-691B-43800
0 US-10-714-333A-84328
0 US-10-714-333A-84328
0 US-10-714-333A-84328
0 US-10-714-333A-860087
0 US-11-093-832-83294
0 US-11-33A-84132-847874
0 US-11-348-413-247875
0 US-11-348-413-248534
0 US-11-348-413-248535
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; Publication No. US20070009899A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
APPLICANT: Wyeth
TITLE OF INVENTION: WODELS OF INFLAMMATORY DIS
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SEQ ID NO 171431
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Best Local Similarity
Matches 10; Conserv
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2: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
3: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
4: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
5: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
6: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
7: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
8: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
7: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
10: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
11: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
12: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
13: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
14: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
15: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
16: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
17: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
18: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
19: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
19: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
19: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
18: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
19: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
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19: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
19: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
18: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
18: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
18: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_
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Sequence 661177,
Sequence 12205, A
Sequence 25233, A
Sequence 2175725,
Sequence 2187318,
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Sequence 928822,
Sequence 1077569,
Sequence 1245669,
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                                                                                                                                                                                                June 19, 2007, 13:01:51 ; Search time 610 Seconds (without alignments) 405.912 Million cell updates/sec
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/EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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                                    GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd.
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0 US-11-093-832-661177

1 US-10-956-160-1323

1 US-10-956-160-2533

US-10-709-691B-2175725

US-10-709-691B-2187318

1 US-10-714-3338-928822

0 US-10-714-3338-1077569
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Listing first 45 summaries
                                                                                                                                                     nucleic search, using sw model
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24
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Match Length
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Maximum DB seq length: 25
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APPLICANT: ROSETA GENOMICS LTD
APPLICANT: Bentwich, Itzhak
APPLICANT: Bentwich, Itzhak
APPLICANT: Avniel, Amir
TITLE OF INVENTION: Bioinformatically Detectable Group of Novel Regulatory Bacterial
TITLE OF INVENTION: and Bacterial Associated Oligonuclectides and Uses Thereof
FILE REPERENCE: Efs23
CURRENT APPLICATION NUMBER: US/10/709,691B
CURRENT APPLICATION NOWER: 2004-05-24
NUMBER OF SEQ ID NOS: 4294815
SOFTWARE: PATENTI VETSION 3.3
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APPLICANT: Wyeth
APPLICANT: Would william M
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
TITLE OF INVENTION: WODELS OF INFLAMMATORY DISEASES
FILE REFERENCE: 031896-044000 (AM101084)
CURRENT APPLICATION NUMBER: US/10/956,160
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 222274
SOFTWARE: Patentin version 3.2
              DETECTING GENE EXPRESSION IN ANIMAL DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 15; DB 11; Length 25;
Pred. No. 8.2e+03;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                          DB 11; Length 25;
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                                                                                                                                                                                                                                                                                                                                                                                         7; Mismatches
TITLE OF INVENTION: William M
TITLE OF INVENTION: MUCLEIC ACID ARRAYS FOR
TITLE OF INVENTION: MODELS OF INFLAMMATORY
FILE REPERENCE: 031896-044000 (AM101084)
CURRENT APPLICATION NUMBER: US/10/956,160
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 222274
SOFTWARE: PALENTIN VEYSION 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25233, Application US/10956160 Publication No. US20070009899A1 GENERAL INFORMATION:
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Best Local Similarity 47.8%;
Matches 11; Conservative 7
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Best Local Similarity 43.5%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                 ; TYPE: DNA; Canis familiaris; ORGANISM: Canis familiaris
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LENGTH: 25
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Pred. No. 7.9e+03;
0; Mismatches 0; Indels
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APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
                                       APPLICANT: Leake, Devin_APPLICANT: Marshall, William APPLICANT: Marshall, William APPLICANT: Scaringe, Stephen TITLE OF INVENTION: Functional and Hyperfunctional siRNA
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100.0%; Pred. No. 7.9e+03;
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                                                                                                                              FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/10/714,333A
CURRENT PILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 661177
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CURRENT APPLICATION NUMBER: US/11/093,832
CURRENT FILING DATE: 2005-03-29
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PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2002-114,333
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Publication No. US20070039072A1
GENERAL INFORMATION:
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PRIOR APPLICATION UMBER: 60/426,137
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 661177
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PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
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100.0%; Pre
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100.0%; Pre
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                 Reynolds, Angela
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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ORGANISM: Homo sapiens
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US-10-714-333A-661177
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ORGANISM:
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TYPE: RNA ORGANISM: Streptococcus pneumoniae R6

US-10-956-160-13205 ; Sequence 13205, Application US/10956160 ; Publication No. US20070009899A1

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US-10-709-691B-2175725

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DB 10; Length 19;
.5e+04;
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                                                                                                                                                                                                    APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaring Structional and Hyperfunctional siRNA
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION WUMBER: US/10/714,333A
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR PLING DATE: 2003-09-10
PRIOR PLING DATE: 2003-09-10
PRIOR PLING DATE: 2003-09-10
PRIOR PLING DATE: 2003-09-10
SROUD NUMBER OF SEQ ID NOS: 1591911
SOPTWARE: Proprietary
SROID NO 928822
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APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Garinge, Stephen
IITLE OF INVENTION: Punctional and Hyperfunctional giRNA
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CURRENT APPLICATION NUMBER: US/10/714,333A
CURRENT APPLICATION NUMBER: US/10/714,333A
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2003-09-10
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFWARE: Proprietary
SEQ ID NO 1077569
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                                               Sequence 928822, Application US/10714333A Publication No. US20070031844A1
                                                                                                                            APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
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Reynolds, Angela
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37.5%;
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Best Local Similarity 37.5.
Best Local Similarity 6, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: RNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333A-1077569
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Best Local Similarity
Matches 15; Conserv
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APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAWIRA, NORIHISA
APPLICANT: KODAWA, YUKIKO
APPLICANT: FUJIWURA, TOWOKO
APPLICANT: FUJIWURA, TOWOKO
APPLICANT: SAHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Anniel, Amir
TITLE OF INVENTION: Bioinformatically Detectable Group of Novel Reg
TITLE OF INVENTION: Bioinformatically Detectable Group of Novel Reg
TITLE OF INVENTION: and Bacterial Associated Oligonucleotides and
FILE REFERENCE: E1823
CURRENT APPLICATION NUMBER: US/10/709,691B
CURRENT FILING DATE: 2004-05-24
NUMBER OF SEQ ID NOS: 4254815
SSCTWARE: PatentIn version 3.3
SEQ ID NO 2187318
LENGTH: 19
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     Length 19;
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Pred. No. 9.8e+03;
9; Mismatches 2; Indels
Score 14.8; DB 8;
Pred. No. 9.8e+03;
                                                                                                                                                                                                                                                                              ; Sequence 2187318, Application US/10709691B
; Publication No. US20070031843A1
; GENERAL INFORMATION
APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: RNA; ORGANISM: Streptococcus pneumoniae R6
US-10-709-691B-2187318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 33285, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
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Query Match
Best Local Similarity 38.9%;
Matches 7; Conservative
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Best Local Similarity 38.9%;
Matches 7; Conservative
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SOFTWARE: Patentin version 3.3
SEQ ID NO 33285
LENCTH: 25
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Matches 9; Conserv
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APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
                                                                   APPLICANT: Dharmacon, Inc.
APPLICANT: Khorova, Anastasia
APPLICANT: Keynolds, Angela
APPLICANT: Leake, Devin Hilliam
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
ITILE OF INVENTION: Functional and Hyperfunctional siRNA
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Pred. No. 1.5e+04;
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0; Mismatches 1
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CURRENT FILING DATE: 2005-03-29
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1077569
                                                                                                                                                                                                                                   FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/093,832
CURRENT FILING DATE: 2005-03-29
FRIOR PRICHED BATE: 2003-11-14
PRICH APPLICATION NUMBER: US/10/114,333
PRICH FILING DATE: 2003-09-10
PRICH APPLICATION NUMBER: 60/502,050
PRICH APPLICATION NUMBER: 60/426,137
PRICH APPLICATION NUMBER: 60/426,137
PRICH FILING DATE: 2003-09-10
PRICH FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: PROPILEATY
LENGTH: 19
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Publication No. US20070039072A1
GENERAL INFORMATION:
928822, Application US/11093832 ton No. US20070039072A1
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Best Local Similarity 93.8%;
Matches 15; Conservative
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Best Local Similarity 37.5
Matches 6; Conservative
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US-11-093-832-928822
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US-11-093-832-1077569
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US-11-093-832-1077569
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Pred. No. 1.5e+04;
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APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
APPLICANT: Scaringe, Stephen
APPLICAN: Scaringe, Stephen
APPLICAN: Staringe, Stephen
APPLICAN: 13499US
                                                                                                 APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Laske, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
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Mismatches
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                                                                                                                                                                                                                                                                    FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/10/714,333A
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1245759, Application US/10714333A Publication No. US20070031844A1 GENERAL INFORMATION:
                           ication US/10714333A
                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
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SOFTWARE: Proprietary
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Best Local Similarity 37.5
Matches 6; Conservative
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Best Local Similarity 37.5
Matches 6; Conservative
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US-10-714-333A-1245669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-714-333A-1245759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-714-333A-1245759/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER SOFTWARE: Propises: SEQ ID NO 1245669
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LENGTH: 19
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RESULT 15

US-11-093-832-1245669/C

is Sequence 124569, Application US/11093832

is Publication No. US20070039072A1

GENERAL INFORMATION:

APPLICANT: Bylonds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Scaringe, Stephen

ITILE OF INVERTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT FILIKO DATE: 2005-03-29

PRIOR APPLICATION NUMBER: 06/502,050

PRIOR APPLICATION NUMBER: 66/426,137

PRIOR FILING DATE: 2003-11-14

PRIOR FILING DATE: 2003-11-14

PRIOR FILING DATE: 2002-11-14

NUMBER: OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

LENGTH: NUMBER: NUMBER:
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Query Match 60.0%; Score 14.4; DB 17; Length 19; Best Local Similarity 37.5%; Pred. No. 1.5e+04; Matches 6; Conservative 9; Mismatches 1; Indels 0; Gaps

TYPE: RNA CORGANISM: Homo sapiens US-11-093-832-1245669 ö

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Search completed: June 19, 2007, 13:30:35 Job time : 611.5 secs

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C 15 C 16 C 17 18 19 19 19 19 19 19 19 19 19 10 24 11 25 11 27 11 28 11 29 11 11 21 21 21 21 21 23 24 11 24 11 27 11 28 11 28 11 29 20 31 21 21 21 21 21 21 21 21 21 2	AUTHORS TITLE JOURNAL COMMENT FEATURES BOUICE
m 6.2.1 Biocceleration Ltd. Biocceleration Ltd. earch time 6876 Seconds (without alignments) 216.548 Million cell updates/sec 24 meters: 35954	results predicted by chance to have a [to the score of the result being printed, of the total score distribution. SUMMARIES SUMMARIES Description AZ775852 AZ775853 AZ775853 AZ775853 AZ775853 AZ77583 M0054A13 AZ77583 AZ77583 M0054A13 AZ77583 AZ77583 M0054A13 AZ77583 AZ77583 M0054A13 AZ77583 AZ77583 AZ77583 M0054A13 AZ77583 AZ77583 AZ77583 M0054A13 AZ77583 AZ77583 AZ77583 M0074106 AU014106 AU014106 AU014106
	Pred. No. is the number of results predic score greater than or equal to the score and is derived by analysis of the total s SUMMARIES Result Query Accre Match Length DB ID 13.4 55.8 25 15 AZ758624 2 12.2 50.8 24 5 CA855024 3 12.2 50.0 23 15 AZ75865 4 12 50.0 23 15 AZ75865 C 5 11.6 48.3 21 15 AZ75883 C 6 11.6 48.3 21 15 AZ75883 C 7 11.2 46.7 21 19 AG202804 C 11 11.2 46.7 22 10 CO788412 C 11 11.2 46.7 22 10 CO788412 C 12 11 45.8 22 1 AU014100

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Gaps

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us-10-604-726a-5136.sizlim25.rst

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when the properties of properties of
/dev_stage="Seedlings"
/clone lib="cDNA Peking library 2, 4 day SCN3"
/clone lib="cortor: pBluescript SK-; cDNA clones from mRNA extracted from Peking roots 2 and 4 days past invasion."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ329650

1M0054A13R Mouse 10kb plasmid UUGCIM library Mus musculus genomic CODE UUGCIM0054A13 R, genomic survey sequence.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030
                                                                                                                                                                                                           Length 24;
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47.1%; Pred. No. 1.2e+06;
iive 6; Mismatches 3;
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Insert Length: 10000 Std Error: 0.00
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/strain="C57BL/6J"
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/clone="UUGC1M0054A13"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
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Fax: 801 585 7177
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Matches 8; Conserv
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KEYWORDS
SOURCE
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AZ329650
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                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of public [4]4732114[gb]AR129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XII.0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode (Genome 47 (2), 380-388 (2004)
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US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
                                                                                                                                                                                                              /clome lib="Mouse 10kb plasmid UUGCiM library" /note="Vector: PMD42nv; Purified genomic DNA from M. /note="Wector: PMD42nv; Purified genomic DNA from M. mborulus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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                                                                                                                                                                                     Coli strain XL10-Gold,
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/mol type="mRNA"
cultivar="peking"
/db xref="taxon:3847"
/clone="D08B11"
/tissue_type="Roots"
          mol_type="genomic DNA"
strain="C57BL/6J"
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Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.
Location/Qualifiers
                                                                            db_xref="taxon:10090"
clone="UUGC2M0009N01"
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                                                                                                                                                    sex="Male"
lab host="E.
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Glycine max
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Matches 10; Conservative
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CA850924
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/done libs-mouse loth plasmid UGGCIM library...
/done libs-mouse loth plasmid UGGCIM library...
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus CS7BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonicleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AP129072.1), a copy-number
with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xili0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pederseen, T., Reilly, M., Rose, M., Rose, R., Tingey, R., von Niederhausern, A. and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
                                                                                                                                                                                     Score 12; DB 15;
Pred. No. 1.5e+06;
6; Mismatches 0;
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Insert Length: 10000 Std Error: 0.00
Plate: 0054 row: A column: 13
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0054A13"
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High quality sequence stop: 23.
Location/Qualifiers
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                                                                                                                                                                                                                                            Conservative
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11 TATTGTCTCC 22
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Fax: 801 585 7177
                                                                                                                                                                                   Query Match
Best Local Similarity
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84112, US
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inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0294J14F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/clone l1b="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G77BL/63 (malle) was obtained from the Jackson
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University of Utah Genome Center
University of Utah
Wm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E.,
84112, USA
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Sciurognathi; Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                          Length 23;
                                                                                                                                                                                  Score 12; DB 15; Length 25.
Pred. No. 1.5e+06;
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Fax: 801 585 7177
Email: ddunmgenetics.utah.edu
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Plate: 0294 row: J column: 14
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Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0294J14"
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11 TATTGTCTCC 22
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/note=_Vector: pDNR-LIB; Site 1: SfilA; Site 2: SfilB; Sample name: ApDT; Plant growth place: UNR INRA-INSA BF21; Sowing date: 03/04/2003; Harvesting date: 12/06/2003; Description: Long photoperiod 16-hr light/8-hr dark at 20.0; no overcrowding; grown on Vicia faba 3-wk old seedlings sown under non sterile condition:; experimental condition: standard, see description"
                                                                                                                      LWADU-411 - C12 ApDT Acyrthosiphon pisum cDNA clone ApDTVIIIC12 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                            Hunter, W., Martinez-Torres, D., Rabbe, Y., Sabater-Munoz, B., Stern, D., Tagu, D. and Wincker, P. An expressed sequence tags database for the pea aphid Acyrthosiphon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
1 (bases 1 to 18)
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Pan troglodytes DNA, clone: RP43-063G02.T7, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue type="digestive track"
/dev stage="adults, parthenogenetic females"
/lab_host="TOP10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMR BiO3P, BP 35327, F-35653 Le Rheu Cedex France
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Best Local Similarity 31.2%; Pred. No. 3.3e+06;
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/organism="Acyrthosiphon pisum"
/mol_type="mRNA"
cultivar="inra-lyon-bf2i 1101"
/db.xref="taxon:7029"
/clone="ApDTVIIIC12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Buchnera) or facultative endosymbionts.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plate: VIII row: C column: 12.
                                                                                                                                                                                                                                                                                    Acyrthosiphon pisum (pea aphid)
Acyrthosiphon pisum
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FORWARD: GCCGCATAAACTTCGTATAGCA
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                                                                                                                                                                                                                                       CN750241.1 GI:47515238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 TCTTTCTCTCTCTC 1
25 TTTCCCTTTCCCCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2004)
Contact: D. Tagu
INRA Rennes
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CN750241/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIS39240 25 bp mRNA linear EST 13-MAY-1999 tp64b08.x1 NCI CGAP Ut3 Homo sapiens cDNA clone IMAGE:2204055 3' similar to TR:040726 Q40726 DNA BINDING PROTEIN ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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"Tab host="DHIOB"
/clone lib="NOI CGAP Ut3"
/note="Organ: uferus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.45 kb. Life Technologies catalog #:
11541-018"
                                                                                                  adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Catarrhini; Hominidae; Homo.
1 (bases 1 to 25)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/organism="Homo sapiens"
/mol_type="mRNA"
/more=ref="texton:9606"
/clone="IMAGE:2204055"
/tissue_type="poorly-differentiated endometrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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44.4%; Pred. No. 2.3e+06;
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Matches 8; Conservat
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AUTHORS
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sequences from obligatory

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Length 18; Indels GSS 06-MAR-2004

6 UCUCUCCUUUCGCCACCU 23

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Length 21; Indels

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end was generated during the R&D process and may have higher chance of clone tracking errors. PRIMERS
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Ambystoma mexicanum cDNA 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 22)
Habbermann, B., Bebin, A.G., Herklotz, S., Volkmer, M., Eckelt, K.,
Pehlke, K., Epperlein, H.H., Schackert, H.K., Wiebe, G. and Tanaka, E.M.
An Ambystoma maxicanum EST sequencing project: Analysis of 17,352
expressed sequence tags from embryonic and regenerating blastema
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/cell type="Includes Neural tube, notochord, somites"
/cell type="Includes Neural tube, notochord, somites"
/clone lib="Stage="Stage 18-22"
/note="vector: pcMvSport6; Site 1: Not1; Site 2: Sal1;
Unnormalized cDNA plasmid library prepared by Invitrogen.
Size fractionated mRNA was polydr primed and cloned into Not1-Sal1 site of pcMvSport6. Bacterial host is
EMDH10B-TONA. Average insert size is 1.5 kB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
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                                                                                                                                                                                                                                                                                                                                      /sex="male"
|cell_type="lymphocytes"
|clone_lib="RP-43 Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CO788412 22 Neural tube (NT) Ambystoma m
NT004A G01 St18-22 Neural tube (NT) Ambystoma m
similar to hypothetical protein, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfotenhauerstrasse 108,01307 Dresden, Germany
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Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 11.2; DB 19;
Pred. No. 3.3e+06;
1; Mismatches 3;
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/organism="Ambystoma mexicanum"
                                                                                                                                                                                                                      1.21
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xrefe"taxon:9598"
/clone="RP43-086J05.T7"
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/db_xref="taxon:8296"
                                                                                                                                                                                           Location/Qualifiers
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56.2%; Preć
                                                                                                                            : pBACe3.6
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CO788412.1 GI:51004383
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Fax: 0049 351 210 1489
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                                                                                Sequencing:
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R.Site 1
R.Site 2
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                                                                                                      LIBRARY
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Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
Direct Submission

Submitted (07-3M-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail:redstone@mail:Kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
T-B:82-42-866-7181, Fax:82-42-866-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
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Clones are derived from the chimpanzee BAC library RP-43 This BAC
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Mammalia, Eutheria, Euarchontoglires, Primates, Haplorrhini,
Catarrhini, Hominidae, Pan.
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                                                                         Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Bun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H. BAC end sequences of Library RP-43 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H. BAC end sequences of Library RP-43
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    dammalia; Butheria; Buarchontoglires; Primates; Haplorrhin;;
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Pan troglodytes DNA, clone: RP43-086J05.T7, genomic survey
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/clone_lib="RP-43 Chimpanzee Male BAC Library"
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/db_xref="taxon:9598"
/clone="RP43-063G02.T7"
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                               Catarrhini, Hominidae, Pan.
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: EcoRI
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AG202804.1 GI:45234979
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R.Site 2
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/clone lib="Schizosaccharomyces pombe late log phase cDNA"
/note="Vector: M13mp19; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
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I toass 1 to 23.
Morimpo, M. and Mita, K.
Identification of expressed sequence tags of Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="Mixed stage fosmid library of P. pacificus var. California" /note="Vector: pEpifos-5 Fosmid vector"
Bukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.

1 (bases 1 to 19)
Srinivasan, J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J. Appabb: an AcedB database for the nematode satellite organism Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
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National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
                                                                                                                                                                                                                                                                                             Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
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Schizosaccharomycetales; Schizosaccharomycetaceae;
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Pred. No. 4e+06;
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/organism="Schizosaccharomyces pombe"
/mol type="mRNA"
/strain="972"
                                                                                                                                                                                       Bvolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemanustr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
                                                                                                                                                                                                                                                                                                                                                                                                                           1. 19
// Organism="Pristionchus pacificus" // Mol type="genomic DNA" / Strain="California" /
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/clone="spc09165"
/sex="h minus"
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Location/Qualifiers
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les 5; Conservation
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15 GTCTCTCTTT 5
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/clone lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 25)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AppaDB: an AcedB database for the nematode satellite organism
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This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
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Neodiplogasteridae, Pristionchus.
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                                                                                                                                                                                                                                                                                                      linear
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
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Organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
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Nucleic Acids Res. 32 (1), D421-D422 (2004)
                                                                        Score 11.2; DB 10;
Pred. No. 3.4e+06;
8; Mismatches 3;
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Similarity 31.2%;
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Fax: 00497071601498
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CDNA
into the SmaI site of MI3mpl9 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jb)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="Schizosaccharomyces pombe late log phase cDNA"/note="Vector: Ml3mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the Smal site of Ml3mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"
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2M0203K13F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0203K13 F, genomic survey sequence.
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Morimyo,M. and Mita,K.
Identification of expressed sequence tags of Schizosaccharomyces
                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Mitsucki Morimyo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nirs.go.jp.
Location/Qualifiers
                                                               (URL, http://www.nirs.go.jp)"
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Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                      45.8%; Score 11; DB 1; Length 22; llarity 30.0%; Pred. No. 4.1e+06; Conservative 8; Mismatches 6; Indels
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/mol_type="mRNA"
/strain="972"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (fission yeast)
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/sex="h minus"
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AZ942905
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 (gif #732114|gp|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Railly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Pred. No. 4.1e+06;
; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
                                                                  Mammalia, Butheria, Buarchontoglires, Glires,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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Fax: 801 585 7177
Email: dduun@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0203 row: K column: 13
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/strain="C57BL/6J"
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clone="UUGC2M0203K13"
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Location/Qualifiers
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CQ005107 Sequence S49071 immunoglobu BD225196 Human pap CS195912 Sequence BD464903 OLIGONUCL CQ534390 Sequence M61813 Human alpha AX159481 Sequence BD460907 OLIGONUCL CQ530394 Sequence BD460907 OLIGONUCL CQ530394 Sequence AS9167 Sequence AS9167 Sequence AS9167 Sequence AS9167 Sequence AS9167 Sequence AS9167 Sequence AS917 Sequence AR073651 Sequence AR073655 Sequence AR073657 Sequence AR104055 Sequence AR104057 Sequence	DNA linear PAT 12-SEP-2005 27. and Ly,N. osing or monitoring auto immune 005; San Francisco, CA	DB 2; Length 50; le+04; le+04; le+04; li Indels 0; Gaps 0; luGCAGA 80; l
22.1 50 2 CQ005107 22.1 60 5 S49071 22.1 61 2 BD225196 22.1 65 2 BD464903 22.1 65 2 BD464903 22.1 65 2 CQ534390 22.1 65 2 CQ534390 22.1 65 2 CQ534390 22.1 65 2 CQ53481 21.9 60 2 BD467993 21.9 66 2 BD467997 21.9 65 2 CQ530394 21.9 66 2 AS9167 21.9 76 2 AS9167 21.9 76 2 AS9173 21.9 76 2 AS9173 21.9 76 2 AS9174 21.9 76 2	ALIGNMENTS AR683427 AR683427 AR683427 AR683427.1 GI:74465197 Unknown. Unclassified. Unclassified. Unclassified. Woodward, R. and I wholgemuth, J. Fry, K., Woodward, R. and I wholgemuth J., Fry, K., Woodward, R. and I wholgemuth J., Fry, K., Woodward, R. and I wholgemuth J., Fry, K., Woodward, R. and I wethods and compositions for diagnosing and chronic inflammatory diseases Patent: Use 5905827-A 2856 14-JUN-2005; Expression Diagnostics, Inc.; So. San Friedle. Location/Qualifiers Location/Qualifiers // Organism="unknown" // Mol_type="genomic DNA"	imilarity 41.0%; Score 21.4; conservative 12.8 Mismatches AGUUGGAAGGGCGUUUGCUUCUGUUUUCUGGAAGGGGCGUUUGCUUCUGUUUUCUGGAAGGGGGTTTTTTTTTT
C C C C C C C C C C C C C C C C C C C	RESULT 1 AR683427 LOCUS DEFINITION SE ACCESSION AR VERSION AR KEYWORDS SOURCE UN ORGANISM UN REFERENCE 1 AUTHORS TITLE AUTHORS FEATURES SOURCE AN OORIGIN	Query Match Best Local S Matches 16 Qy 42 2 Qy 42 1 Db 1 1 RESULT 2 AR824195 LOCUS LOCUS DEFINITION See ACCESSION ARR VERSION KRYWORDS SOURCE Union
GenCore version 6.2.1 Copyright (c) 1993 - 2007 Biocceleration Ltd. Lic - nucleic search, using sw model June 19, 2007, 15:44:15; Search time 10160 Seconds (without alignments) 578.270 Million cell updates/sec US-10-604-726A-6033 score: 85 table: US-10-604-726A-6033 table: 1ggguuaucugcaacugagaguuuucuggaugcagaguccu 85 cable: 1ggguuaucugcaacugagag	GenEmbl:* 1: gb_env:* 2: gb_pat:* 3: gb_ph:* 4: gb_pl:* 5: gb_pr:* 6: gb_ro:* 7: gb_sts:* 8: gb_sy:* 9: gb_un:* 11: gb_ov:* 11: gb_ov:* 12: gb_htg:* 13: gb_in:* 14: gb_ow:* 15: gb_ba:* 15: gb_ba:* 15: gb_ba:* 16: gb_ow:* 17: gb_in:* 18: gb_in:* 18: gb_in:* 18: gb_in:* 18: gb_in:* 19: gb_in:* 18: gb_in:* 18: gb_in:* 18: gb_in:* 19: gb_in:* 18: gb_in:* 19: gb_in:* 10: gb_in:* 10: gb_in:* 10: gb_in:*	25.2 50 2 AR663427 24.5 76 2 BD437654 24.5 76 2 BD437654 24.5 76 10 AY4723081 23.5 60 2 CQ539417 23.3 83 2 AX982586 23.3 83 2 AX982586 23.3 83 2 AX982586 23.3 83 2 AX982586 22.6 60 2 CQ539417 22.6 60 2 CQ539417 22.6 60 2 CQ53947 22.6 65 2 BD47569 22.6 65 2 BD487569 22.4 50 2 AR826843 22.4 50 2 AR826843 22.4 50 2 AR826843 22.4 50 2 AR826843 22.5 6 65 2 CQ557056
OM nucleic - nu Run on: Title: Perfect score: Sequence: Scoring table: Scarched: Total number of Minimum DB seq Maximum DB seq	Database : Pred. Pred. Result	'

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Gaps

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VRL 22-FEB-2002

AUTHORS TITLE

JOURNAL

FEATURES

REFERENCE

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Human immunodeficiency virus 1 (HIV-1)
Human immunodeficiency virus 1
Viruses; Retro-transcribing viruses; Retroviridae;
Orthoretrovirinae; Lentivirus; Primate lentivirus group.
1 (bases 1 to 76)
Scriba,T.J., de Villiers,T., Treurnicht,F.K., zur Megede,J.,
Barnett,S.W., Engelbrecht,S. and van Rensburg,E.J.
Characterization of the South African HIV type 1 subtype C complete
5' long terminal repeat, nef, and regulatory genes
AIDS Res. Hum. Retroviruses 18 (2), 149-159 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scriba,T.J., de Villiers,T., Treurnicht,F.K., zur Megede,J., Scriba,T.J., de Villiers,T., Treurnicht,F.K., zur Megede,J., Barnett,S., Engelbrecht,S. and Janse van Rensburg,E.
Direct Submission Submitted (04-JUL-2001) Department of Medical Virology, University of Stellenbosch, PO Box 19063, Tygerberg, Western Cape 7505, South
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 UGAGAGGGGCUGGUUAAGGCGUCCCCAAGUUGGAAGGGCGCUTUGCUUCUGUUUUC 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           zur Megede,J., Barnett,S.W., Engelbrecht,S. and van Rensbur
Polynucleotides encoding antigenic hiv type c polypeptides,
polypeptides and uses thereof
Patent: WO 0204493-A 73 17-JAN-2002;
CHIRON CORPORATION (US) ; University of Stellenbosch (ZA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV-1 TV001 from South Africa Rev (rev) gene, exon 1. AY047230
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/organism="Human immunodeficiency virus 1"
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="texon:34530"
/noTe="HIV Type C RevExon1 Wild Type"
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41.1%; Pred. No. 2.2e+04;
tive 11; Mismatches 22
                                  other sequences; artificial sequences.
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/isolate="TV001"
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/country="South Africa"
/note="gubtype: C"
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Best Local Similarity 41.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLYPEPTIDES AND USES THEREOF.
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PD 29-JAN-2004
    1 (bases 1 to 50)
Wohlgemuth, J., Fry, K., Woodward, R. and Ly, N.
Methods and compositions for diagnosing and monitoring transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 UGAGAGGGGCUGGUUAAGGCGUCCCCAAGUUGGAAGGGCGCUUUGCUUCUGUUUUC
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                                                                                                                                                                                                                                                                       Query Match 25.2%; Score 21.4; DB 2; Length 50; Best Local Similarity 41.0%; Pred. No. 1.3e+04; Matches 16; Conservative 12; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 76;
                                                              Patent: US 7026121-A 2856 11-APR-2006;
Expression Diagnostics, Inc.; South San Francisco,
US;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 24.5%; Score 20.8; DB 2; Length 7 1 Similarity 41.1%; Pred. No. 2.2e+04; 23; Conservative 11; Mismatches 22; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           susan w barnett, jan zur megede, esutorerita
                                                                                                                                                                                                                                                                                                                                                                                    1 AGTCCCAAGGGTGTTTTGTTACTGTTTTCTCCCATGAATA 39
                                                                                                                                                                                                                                                                                                                                                            42 AGUUGGAAGGCCCUUUGCUUCUGUUUUCUGGAUGCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        susan enjeruburehito
Description of Artificial Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BD437654.1 GI:92321646
JP 2004502445-A/64.
synthetic construct
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 76)
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Sequence 73 from Patent WO0204493.
AX455957.1 GI:21714941
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                                                                                                                                                                                                           /mol_type="genomic DNA"
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05-JUL-2000 US 09/6103
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                                                                                                                                                                  1. .50
/organism="unknown"
                                                                                                                                              Location/Qualifiers
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Best Local S:
Matches 23
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AUTHORS TITLE

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PAT 15-JAN-2004

VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

JOURNAL

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RESULT 6 BD469930

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linear PAT 18-SEP-2002
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Buarchontoglires; Primates; Haplorrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GGUUAUCUGCAACUGAGAGGGCUGGUUAAGGCGUCCCCAAGUUGGAAGGGCGCUUUGCU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 GGGCACCTGCCTAGAGGGTAGGGTGGAAACTCCATCCCCAATGAGCACGGGCTCATCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00,
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JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN
                                                                                                                                                                                                                                                                                                                                                                                                                                 Dumas Milne Edwards, J.B., Jobert, S. and Giordano, J.Y.
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Indels
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1 (bases 1 to 83)
Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.
EST and encoded human protein
GENETH: JP 2002010789-A 9522 15-JAN-2002;
GENSET CORP
10;
                                     78
                                                                  25 GTTGGAAGACGGATTTGCTTTGGTATTCTGCTTCCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 19.8; DB 2;
Pred. No. 5.3e+04;
8; Mismatches 32;
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Patent: EP 1104808-A 13389 06-JUN-2001;
Genset (FR)
                                                                                                                                                                                         AX982586 83 bp DNA
Sequence 13389 from Patent EP1104808.
                                         GUUGGAAGGCCCUUUGCUUCUGUUUUCUGGAUGCA
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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BD117445
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05-AUG-1999 US 60/1474
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JP 2002010789-A/9522
15-JAN-2002
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JP 2002010789-A/9522.
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23.3%;
Best Local Similarity 43.7%;
Matches 31; Conservative 8
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Homo sapiens
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Homo sapiens
Conservative
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GCTGGTTCCCG 76
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C12N15/
14;
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AX982586
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                                                                               BD469930 60 bp DNA linear PAT 04-NOV-2005 OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE VARIANTS THAT POPULATE A TRANSCRIPTOME.
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Mammalia; Butheria; Buarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Buarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                      Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S. OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE VARIANTS THAT POPULATE A TRANSCRIPTOME PATENT: JP 2004508019-A 9052 18-MAR-2004; Avi SHOSHAN, Alon WASSERMAN, Eli MINTZ, Liat MINTZ, Simchon FAIGLER
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chon PI
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20-JUL-2001 JP 2002516365
02-MAY-2001 US 60/287724,28-JUL-2000 US 60/22
shoshan,alon wasserman,eli mintz,liat mintz,simchon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 GUUGGAAGGGCGCUUUGCUUCUGUUUUCUGGAUGCA 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            variants that populate a transcriptome
Patent: WO 0210449-A 9052 07-FEB-2002;
Compugen Inc. (US)
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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JP 2004508019-A/9052
                                                                                                                                                                   BD469930.1 GI:92319490
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                                                                                                                                                                                  JP 2004508019-A/9052.
Homo sapiens (human)
Homo sapiens
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CC
FH Key
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RESULT 7 CQ539417 LOCUS DEFINITION

Matches

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<1. .>60
/gene="BV6S5-BJ1S5"
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1 (bases 1 to 60)
                                                                                                                                             Location/Qualifiers
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Nucleic Acids and Encoded Polypeptides Associated with Bipolar Disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 GGGCACCTGCCTAGAGGGTAGGGTAGAACTCCATCCCCAATGAGGCACGGGCTCATCTCT 65
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Mammalia, Eutheria, Euarchontoglires, Primates, Haplorrhini,
                                                                                                                                                                                        GGUUAUCUGCAACUGAGAGGGCCUGGUUAAGGCGUCCCCAAGUUGGAAGGGCCCCUTUGCU 61
                                                                                                                                                                                                        2 GEUDAUCUGCAACUGAGAGGGGUGGUDAAGGCGUCCCCAAGUUGGAAGGCCCUTUGCU
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                          organism='Homo sapiens (human)'.
                                                                                                                                   Length 83;
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                                                                                                                                                               32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Unknown.
Unclassified.
1 (Dases 1 to 83)
Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
EST's and encoded human proteins
Parent: US 6639063-A 13389 28-OCT-2003;
Genset S.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 23.3%; Score 19.8; DB 2; Best Local Similarity 43.7%; Pred. No. 5.3e+04; Matches 31; Conservative 8; Mismatches 32;
                                                                                                                                     DB 2;
  Location/Qualifiers
                                                                                                                                Score 19.8; DB 2;
Pred. No. 5.3e+04;
8; Mismatches 32
                                                                                                                                                                                                                                                                                                                                       AR421892 83 bp DNA Sequence 13389 from patent US 6639063. AR421892

    .83
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/organism="unknown"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Catarrhini; Hominidae; Homo.
1 (bases 1 to 51)
                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DD162947.1 GI:83974587
JP 2005508618-A/41.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                               AR421892.1 GI:40177002
                                                                                                                                     23.3%;
                                                                                                                                                               31; Conservative
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66 GCTGGTTCCCG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 UCUGUUUUCUG 72
                                                                                                                                                                                                                                                             |:| :: | |
GCTGGTTCCCG 76
                                                                                                                                                                                                                                            UCUGUUUUCUG 72
                                                                                                                                                  Local Similarity
     Key
source
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DD162947
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AF011577 60 bp mRNA linear PRI 21-JAN-1998
Homo sapiens T cell receptor beta chain (BV6S5-BJ1S5) mRNA, partial
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Highly biased CDR3 usage in restricted sets of beta chain variable regions during viral superantigen 9 response
J. Exp. Med. 187 (2), 253-258 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Haplorrhini,
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Ciurli, C., Sekaly, R.-P. and Denis, F.
Direct Submission
Submitted (01-JUL-1997) Immunology, IRCM, 110 Pine Avenue West, Montreal, Quebec H2W 1R7, Canada
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rowen, L., Koop, B.F. and Hood, L. The complete 685-kilobase DNA sequence of the human beta T cell
Nucleic Acids and Encoded Polypeptides Associated with Bipolar Patent: JP 2005508618-A 41 07-APR-2005;
Egea Biosciences Inc.
OS Homo sapiens
PN JP 2005508618-A/41
PD 07-APR-2005
PF 02-AUG-2002 JP 2003517242
PR 02-AUG-2001 US 09/922255
PI glenn a evans
CC
FH Key Location/Qualifiers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 GGGCGCUUUGCUUCUGUUUCUGGAUGCAGAGUC
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    .51
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/db_xref="taxon:9606"

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/organism="Homo sapiens"
/mol_type="mRNA"
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/gene="BV6S5-BJ1S5"
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Search completed: June 19, 2007, 18:35:09 Job time : 10162 secs
                                                                                                                                                                                                                                                                                                                                                                                                                     Unclassified.
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Best Local Similarity
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Best Local S
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TITLE
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 65)
Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.
Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.
OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
VARIANTS THAT POPULATE A TRANSCRIPTOME
Patent: JP 2004508019-A 26691 18-MAR-2004;
Avi SHOSHAN, Alon WASSERWAN, Bli MINTZ, Liat MINTZ, Simchon FAIGLER
                                                                                                                                                                                                                              65 bp DNA linear PAT 04-NOV-20
OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
VARIANTS THAT POPULATE A TRANSCRIPTOME.
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Patent: WO 0210449-A 26691 07-FEB-2002;
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18-MAR-2004
20-JUL-2001 JP 2002516365
02-MAY-2001 US 60/287724,28-JUL-2000 US 60/221607
shoshan,alon wasserman,eli mintz,liat mintz,simchon PI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.6%; Score 19.2; DB 2; Length 65; 41.7%; Pred. No. 9.2e+04; ive 10; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="BV6S5-BJ1S5"
/note="T cell receptor junctional region"
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                                                                                                    13; Indels
                                                                   Length
                                                                                                                                    73
                                                                                                                                                     34 CGUCCCCAAGUUGGAAGGGCGCUUUGCUUCUGUUUUCUGG
                                                                  Score 19.2; DB 5;
Pred. No. 9.2e+04;
9; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="unassigned DNA"
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    .65
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                                                                                                                                                                                                                                                                                                               BD487569.1 GI:92356846
JP 2004508019-A/26691.
                                                                                                                                                                                                                                                                                                                                                                                 unclassified sequences.
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                                                              22.6%;
45.0%;
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Matches 20; Conservative
                                                                                                  18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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                                                                                 Best Local Similarity
Matches 18; Conserva
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                                                                                                                                                                                                                  RESULT 13
BD487569
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TITLE
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CQ557056
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TITLE
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Wohlgemuth, J., Fry, K., Woodward, R. and Ly, N.
Methods and compositions for diagnosing or monitoring auto immune
and chronic inflammatory diseases
Patent: US 6905827-A 5504 14-JUN-2005;
Expression Diagnostics, Inc.; So. San Francisco, CA
                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                     Length 65;
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                                                                                                                                   1 Similarity 41.7%; Pred. No. 9.2e+04; 20; Conservative 10; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 19; DB 2; I Pred. No. 1.1e+05; 10; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                    AR686075 504 from patent US 6905827.
AR686075

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Location/Qualifiers
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			18	18.6	21.
	GenCore version 6.2.1		19	18.6	21.
	Copyright (c) 1993 - 2007 Biocceleration Ltd.	U	20	18.6	21.
		υ	21	18.6	21.
		U	22	18.6	21.
OM nucleic - nu	OM nucleic - nucleic search, using sw model	U	23	18.6	21.
		υ	24	18.4	27
Run on:	June 19, 2007, 15:35:52; Search time 314 Seconds		25	18.4	21.
	(without alignments)	υ	56	18.4	21.
·	2006.045 Million cell updates/sec		27	18.4	21.
			28	18.4	21.
Title:	US-10-604-726A-6033		59	18.4	21.
Perfect score:			30	18.4	27
Sequence:	1 ggguuaucugcaacugagaguuuucuggaugcagaguccu 85		31	18.4	21.
			32	18.4	21.
Scoring table:	IDENTITY NUC	υ	33	18.4	21.
ì	Gapop 10.0 , Gapext 1.0	υ	34	18.4	21.
		U	32	18.2	21.
Searched:	5620219 segs, 3705283702 residues	υ	36	18.2	21.
		U	37	18.2	21.
Total number of	Total number of hits satisfying chosen parameters: 6044068		38	18.2	21.
			39	18.2	21.
Minimum DB seg length: 0	length: 0	υ	. 04	18.2	21.
Maximum DB seg length: 85	length: 85	υ	41	18.2	21.
		U	42	18.2	21.
Post-processing	Post-processing: Minimum Match 0%		43	18.2	21.

Ae167275 Murray re
Ae169636 Murray re
Abn27281 Rat splic
Aa421804 Human gen
Aag85150 Ureaplasm
Aag8519 Ureaplasm
Aag85119 Ureaplasm
Aag85119 Ureaplasm
Aag85138 Ureaplasm
Aag86310 Hematolog
Ae157607 SARS coro
Aet88275 M17 synth
Ady93938 Codon opt
Ady93938 Comamonas
Ac68089 Comamonas
Ae18849 C. testos
Ac695017 Human col
Abn32231 Human spl
Aed19289 E. coli s
Abn3231 Human spl
Abn36415 Mouse splic

Aei67892 DNA encod Ado70341 PCR prime Abn88696 E2F aptam

AED19289 ABN58415 ABN30268 AEI 67892 ADO70341 ABN88696

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_200701:* geneseqn1980s:* geneseqn1990s:*

Database :

geneseqn2000s:* geneseqn2001as:* geneseqn2001bs:*

geneseqn2003cs: geneseqn2003ds geneseqn2004as geneseqn2004bs

geneseqn2003as:

geneseqn2003bs:

genesean2002bs:

geneseqn2002as:

	0.00	DECITION 1
	ABZ	ABZ02865 ID ABZ02865 standard, DNA, 50 BP.
	X Z i	ABZ02865;
•	첫 E ⁻	09-JAN-2003 (first entry)
	Z 23 :	Human leukocyte gene expression profiling probe SEQ ID NO 2856.
	X & S	T7; leukocyte; gene expression profiling; allograft rejection;
	2 2 3	eroscielosis, congestive meatr failure, systemic umatoid arthritis, osteoarthritis, cytomegaloviru
	ž×	
	8	Homo sapiens.
	XX	WO200257414-A2.
	XX CL	25-JUL-2002.
	Χ'n	22-OCT-2001; 2001WO-US047856.
	X 8	28-0CT-2000: 200011S-0241994B
	: E	
	X & S	(BIOC-) BIOCARDIA INC.
	X II X	muth J, Fry K, Matcuk G, Altman P,
	ZX	Ly N, Woodward K, Quercermous I, Johnson F;
	DR X	WPI; 2002-636525/68.
	\$ E	New system for leukocyte expression profiling, diagnosing a disease,
	PT	<pre>monitoring (the rate of) progression of a disease, e.g. atheroscleros or congestive heart failure, comprises diagnostic oligonucleotides.</pre>
	XX SS	Claim 1; Page 418; Opp; English.
	¥8	The invention relates to a system for detecting gene expression, which
	;	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2007s:

geneseqn2005s: geneseqn2006s: SUMMARIES

Query Match Length DB

Score

Result g or

Aec75978 Cancer pr Aej81361 Human cDN Ael30539 Human SNP Ael30538 Human SNP Aex33875 HPV-16 in Abn31277 Ret splic Adz27768 Chemosens

AAX33875 ABN31277 ADZ27768

Abz02865 Human leu Abl3994 Wild type Adm3807 HIV-1 pol Abn36304 Human spl Adk19849 Human man Adk19849 Type IIs Aek61465 Secreted Abn53943 Mouse spl Adm95921 Rat antis Abz05513 Human leu

ADK19849 ADK19487

AEK61465

ADM73807 ABN36304

ABN53943 ADM95921 ABZ05513 AEC75978

221.4 200.8

AEJ81361

Description

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gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful for leukcoyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus,
comprises one or two isolated DNA molecules that detect expression of a
                                                                                                                                                                                                                                                                                                                     rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
   8X88888888888X8
```

Sequence 50 BP; 12 A; 10 C; 9 G; 19 T; 0 U; 0 Other;

ö 25.2%; Score 21.4; DB 6; Length 50; 41.0%; Pred. No. 6.1e+02; tive 12; Mismatches 11; Indels 42 AGUUGGAAGGCCCUUUGCUUCUGUUUUCUGGAUGCAGA 80 16; Conservative Local Similarity Query Match Matches ò a

BP ABL39994 standard; DNA; 76 ABL39994;

Human immunodeficiency virus type C; antigenic HIV type C protein; immunogenic; immunisation; gag; pol; vif; vpr; tat; rev; vpu; env; nef; immunostimulant; gene therapy; gene; ds. Wild type 8_5_TV1_C.ZA exon 1 of Rev polynucleotide SEQ ID NO:73 (revised)
(first entry) 29-AUG-2003 15-MAY-2002

Human immunodeficiency virus; type C.

WO200204493-A2

17-JAN-2002.

05-JUL-2001; 2001WO-US021241.

05-JUL-2000; 2000US-00610313.

(UYST-) UNIV STELLENBOSCH. CHIR) CHIRON CORP.

Van Rensburg EJ; Engelbrecht S, Zur Megede J, Barnett SW, WPI; 2002-154920/20. New polynucleotides encoding antigenic HIV Type C polypeptides, useful applications including DNA immunization or generation of packaging cell lines, particularly in gene therapy.

Example 1; Fig 44; 233pp; English.

The present invention describes expression cassettes comprising a polymorlectide sequence encoding a polympetide comprising immunogenic HIV type C polypeptides. The expression cassettes comprise any of the HIV type C polypeptides. The expression cassettes comprise any of the HIV type C sequences encoding Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env or Nef (I). (I) have immunostimulant activity and can be used in gene therapy. The HIV type C polymorlectides are useful in applications including DNA immunisation, generation of packaging cell lines, and production of HIV Type C proteins The polymuclectides are particularly useful in gene Herapy and DNA immunisation applications. ABL19991 to ABL40054 and ABB06215 represent sequences used in the exemplification of the present invention. (Updated on 29-AUG-2003 to standardise OS field)

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Gaps
                                                  ö
                         Length 76;
                                                  Indela
20 G; 11 T; 0 U; 0 Other;
                       24.5%; Score 20.8; DB 6;
41.1%; Pred. No. 1.2e+03;
ative 11; Mismatches 22;
 ΰ
                                                     23; Conservative
 Sequence 76 BP; 27 A; 18
                                       Local Similarity
                           Query Match
                                                     Matches
                                          Best
  g
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15 UGAGAGGGGCUGGUUAAGGCGUCCCCAAGUUGGAAGGGCGCUUUGCUUCUGUUUUC 70 셤 ò

HIV-1; gene; ds; HIV pol; immune response; DNA immunisation; HIV type C protein; immunostimulant. ADM73807 standard; DNA; 76 BP. 03-JUN-2004 (first entry) HIV-1 polynucleotide #42. ADM73807; RESULT 3 ADM73807/c

Human immunodeficiency virus 1. 05-JUL-2001; 2001US-00899575. US2003223961-A1 04-DEC-2003.

05-JUL-2000; 2000US-00610313. RENSBURG E J V. ς. (MEGE/) MEGEDE J Z. (BARN/) BARNETT S W. (ENGE/) ENGELBRECHT (RENS/)

Rensburg EJV; Engelbrecht S, Megede JZ, Barnett SW,

WPI; 2004-060515/06.

New expression cassette comprising a polynucleotide sequence encoding an HIV Pol polypeptide, useful in eliciting an immune response, in DNA immunization, generating of packaging cell lines or in producing HIV Type proteins

Example 1; SEQ ID NO 73; 160pp; English

The invention relates to an expression cassette comprising a polynucleotide sequence encoding an HIV Pol polypeptide. The invention also relates to a recombinant expression system for use in a host cell comprising an expression cassette, where the polynucleotide sequence further comprises control elements capable of driving expression in the selected host cell, a cell comprising an expression cassette where the polynucleotide sequence further comprises control elements compatible with the expression in the cell and a composition for generating an immunological response, comprising an expression cassette. The expression cassette and the methods of the invention are useful in eliciting an immune response, in DNA immunisation, in generation of packaging cell lines and in producing HIV Type C proteins. This sequence represents an HIV-1 polynucleotide of the invention.

Sequence 76 BP; 27 A; 18 C; 20 G; 11 T; 0 U; 0 Other;

Gaps ö DB 12; Length 76; 22; Indels 24.5%; Score 20.8; DB 12 41.1%; Pred. No. 1.2e+03; 11; Mismatches Local Similarity 41.13 tes 23; Conservative Query Match Matches

ö

UGAGAGGGCUGGUUAAGGCGUCCCCAAGUUGGAAGGGCGCUTUGCUUCUGUUUUC 70 15

> 8 셤

human; mannosyl transferase; antimanic; antidepressant; gene therapy; fusion protein; chromosome 9 fusion protein; chromosome 11 translocation; bipolar disorder; single nucleotide polymorphism; SNP; ds.

Human mannosyl transferase-related SNP region DNA SeqID51.

(first entry)

06-MAY-2004

ADK19849;

ADK19849 standard; DNA; 51 BP.

RESULT 5 ADK19849 /*tag= a /standard_name= "Single_nucleotide_polymorphism"

Location/Qualifiers

Homo sapiens

replace (26,G)

variation

02-AUG-2002; 2002WO-US024490. 02-AUG-2001; 2001US-0092225. (EGEA-) EGEA BIOSCIENCES INC.

WO2003012064-A2

WPI; 2003-268116/26.

Evans GA;

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messenger RNAs that populate a (sub-)transcriptome, where the sub-
C transcriptome comprises messenger RNAs transcribed from multiple
transcription units that populate a genome. The library comprises several
coligonucleotides, each capable of hybridising selectively to a set of
messenger RNAs transcribed from a given transcription unit of the genome,
which encodes one or more messenger RNA splice variants. The
coligonucleotide libraries are useful for detecting mRNAs from a
biological sample, in expression profiling studies, in qualitatively or
cymanticatively characterising the corresponding transcriptome, and in
chetcting RNA transcripts and splice variants of human or animal
transcriptomes. The libraries may also be used as specialised mini
colipogical or detect transcripts of a sub-transcriptome under a particular
biological or pathological state, and so allowing the detection of tissue
and pathology-specific genes such as those genes only expressed in
specific tissue under a specific pathological condition; to detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ಹ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rats, humans and mice, which are used in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of genome, useful for detecting tissue-, pathology-, and developmental-specific genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention describes oligonucleotide libraries for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     developmental specific genes; and to detect RNA transcripts and splice
                                                                                                                                                 Human spliced transcript detection oligonucleotide SEQ ID NO:9052
                                                                                                                                                                                         Human, mouse, rat, splice transcript, detection, RNA transcript, splice variant, transcriptome, oligonucleotide library, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.5%; Score 20; DB 6; Length 60; 38.9%; Pred. No. 2.2e+03; ive 12; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Faigler S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 60 BP; 12 A; 9 C; 21 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mintz L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID NO 9052; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mintz E,
                 ABN36304 standard; DNA; 60 BP
                                                                                                                                                                                                                                                                                                                                                                                       20-JUL-2001; 2001WO-IB001903.
                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JUL-2000; 2000US-0221607P.
02-MAY-2001; 2001US-0287724P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shoshan A, Wasserman A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (COMP-) COMPUGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-257383/30.
                                                                                                                                                                                                                                                                                                       WO200210449-A2
                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                      15-JUL-2002
                                                                                                                                                                                                                                                                                                                                               07-FEB-2002
                                                            ABN36304;
ABN36304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to a novel isolated protein which comprises a human mannosyl transferase having the same sequence as the fully defined oli- or 255-amino acid sequence or its fragment. The invention may be useful for the production of compounds with an antimanic or antidepressant activity whilst the disclosed sequences may be used for gene therapy. The invention also provides a human mannosyl transferase fusion protein and a chromosome 9 fusion protein, both of which result from a chromosome 11 translocation. The human mannosyl transferase and the fusion protein are useful for diagnoshing or predicting the modulates the activity of a mannosyl transferase. The present sequence is that of a region of human DNA surrounding a single nucleotide than invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptide comprising human mannosyl transferase, useful for diagnosing or predicting the susceptibility to a bipolar disorder identifying a compound that modulates the activity of a mannosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 51 BP; 7 A; 12 C; 9 G; 23 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.1%; Score 19.6; DB 10;
35.3%; Pred. No. 2.9e+03;
iive 13; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGCGCUUUGCUCUGUUUCUGGAUGCAGAGUC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         || |-::: :: ::::|||:|
|GGCACCTTTTTTTTTTTTTGGATACAGAGTC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; SEQ ID NO 51; 147pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADK19487 standard; DNA; 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
hes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADK19487
ID ADK1
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
엄
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Gaps

.; 0

43 GUUGGAAGGGCGCUUUGCUUCUGUUUUCUGGAUGCA 78

25

8

14; Conservative

Best Local Similarity Matches 14; Conserv

Query Match

EP1314783-A1

ADK19487;

(first entry) 06-MAY-2004 Type IIs restriction enzyme construct #10.

recognition site; type IIS restriction enzyme; nucleic acid library; ligation; ss.

Unidentified

28-MAY-2003

22-NOV-2001; 2001EP-00127864

2001EP-00127864. 22-NOV-2001; (SLON-) SLONING BIOTECHNOLOGY GMBH.

O'connell T; Schatz O,

WPI; 2003-451033/43.

New single-stranded nucleic acid, useful in parallel production of synthetic genes, includes a sequence containing type IIS enzyme recognition site and a defined sequence.

Disclosure; Fig 7; 69pp; German.

This invention describes the novel use of a single-stranded nucleic acid, tor use in preparation of nucleic acid comprising a part (A) comprising the sequence of a recognition site for a type IIS restriction enzyme, or the sequence of a recognition site for a type IIS restriction enzyme, or the formula of comprises preparing an oligomuclectide (ONI), optionally by modification of an oligomuclectide linked to a surface, that contains the recognition site for fragment or complement) of a type IIS enzyme that cuts outside its recognition sequence to generate a single-stranded overhang. ONI is ligated with the single-stranded nucleic acid, particularly where part (A) is complementary to the overhang, to form a 5'-overhang, which is filled in. A second oligomucleotide (ONZ), comm a 5'-overhang, which is filled in. A second oligomucleotide (ONZ), comm a 5'-overhang, which is filled in. A second oligomucleotide (ONZ), complementary to the overhang and comple-stranded oligomucleotides (ONI) onl) with a 3'-overhang and constrained by part (A) complementary to the single-stranded nucleic acid consisting of part (A) complementary to the single-stranded nucleic acid consisting of part (A) complementary to the single-stranded nucleic acid, their same for all members of a group, and a 2 or 3-nf (B) that is different for each member of the agroup, and a 2 or 3-nf (B) that is different for each member of the group of this seep are then cleaved with the type IIS enzyme that is product from one group ligated with those of the other group. The groups of single-stranded nucleic acid, their 5'-ends filled in and the product from one group ligated with those of the other group. The margner recognition site for coupling to a matrix. The enzyme recognition of the method comprises ligating two partially and the overhang or entirely in the overhang or entirely in the double-stranded region of ONIO was only with 5'-overhang sof 3 nt which in the overhang or entirely in the encognition site for type IIS enzyme same for matrix. The enzyme ON21 type. The same process is used to produce another ONe and the two final ONe are ligated in an orientation determined by blockade of the ends that are not intended for ligation. The product of this step is then cleaved with an type IIS enzyme that cuts in either of the ONe. The enzyme used creates a 3 nt overhang, except in the last repetition of the process leading to ONe, where it creates an overhang of other than 3 nt. the product cleaved with the enzyme appropriate for ON21 and the resulting extended oligonucleotide (ONe) is separated and optionally the procedure repeated sequentially with additional oligonucleotides of the

The nucleic acids are used to prepare nucleic acids, particularly synthetic genes, or nucleic acid libraries, particularly by sequential ligation of oligonucleotides in parallel reactors, in sequence-independent manner. The products of the invention makes possible sequence-independent nanner. The products of the invention makes possible sequence transfer components, i.e. an oligonucleotide library of relatively low complexity. This reduces the effort involved in producing a complete library of sequences, without problems of low ligation efficiency associated with 1 or 2 nucleotide overhangs, and the use of short oligonucleotides improves both yield and purity. The proportion of broken and failed sequences is reduced and many gene variants can be prepared simultaneously. This sequence represents a polynucleotide used to make the Type IIS restriction enzyme constructs used to illustrate the method of the invention. \$

21 T; 0 U; 0 Other; ö 21 Sequence 74 BP; 10 A; 22 C;

Gaps ö DB 10; Length 74; Indels Pred. No. 3.3e+03; 7; Mismatches 19; Score 19.6; 23.1%; 48.0%; 24; Conservative Local Similarity Query Match Matches

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62 15 UGAGAGGCCUGGUUAAGGCGUCCCCAAGUUGGAAGGGCGCUUUGCUUCU 64 13 TGAGACGCGCTTTTGCGCGTCTCACCAAGTCGTAAGAGCGCGCGGCGTTT ò g

RESULT 7 AEK61465

AEK61465 standard; DNA; 60

AEK61465;

30-NOV-2006 (first entry)

Secreted soluble agrin variant PCR primer SEQ ID NO 8.

protein engineering; muscular-gen.; nootropic; neuroleptic; neuroprotective; enzyme inhibition; screening; atrophy; schizophrenia; cognitive disorder; head injury; cerebroprotective; vulnerary; neurological disease; cerebrovascular ischemia; vasotropic; multiple sclerosis; parkinsons disease; antiparkinsonian; Alzheimers disease; agrin; PCR; primer; ss

Synthetic

Unidentified.

WO2006103261-A2.

05-OCT-2006.

29-MAR-2006; 2006WO-EP061152.

2005EP-00102481. 30-MAR-2005;

(UYZU-) UNIV ZUERICH.

P, Hettwer S, Bolliger MF, Reif R, Sales S; Sonderegger P, Luescher D, Re

ä

Kunz

Dreier B,

WPI; 2006-670399/69.

Determining neurotrypsin inhibitor compound involves incubating compour with neurotrypsin having protease domain, and agrin peptide comprising specified cleavage site; in aqueous buffer, and measuring amount of cleavage of agrin.

Example 20; SEQ ID NO 8; 91pp; English.

The invention describes a method of determining a neurotrypsin inhibitor compound involves: (a) incubating the compound with neurotrypsin, its variant or fragment comprising the protease domain of neurotrypsin, and protein or peptide comprising agrin, its variant or fragment comprising cleavage site between arginine 995 and alanine 996, or lysine 1754 and

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catalytic activity of neurotrypsin involving: incubating neurotrypsin, its variant or fragment comprising the protease domain with a protein or peptide comprising agrin, its variant or fragment comprising the cleavage site of agrin, in an aqueous buffer solution; and mesuring the amount of cleavage of agrin, and neurotrypsin inhibitor compounds of formula (I) and its addition salts. The method is useful for: determining a prophylaxis of diseases caused by deficiency of synapses, skeletal muscle atrophy, schizophrenia and conjulive disturbance; for measuring catalytic activity of neurotrypsin; and for impairment of cognitive functions in patients with Alzheimer's disease, Parkinson's disease, multiple
      ö
                                                                                                                                                                                                                                                                                                                                                                                                 sclerosis, stroke, and head trauma. This sequence represents a primer used in the creation of an engineered secreted soluble agrin variant.
   serine 1755; in an aqueous buffer solution; and measuring the amount cleavage of agrin. Also described are: a method (M1) for measuring
8833333333333333333
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Sequence 60 BP; 8 A; 16 C; 19 G; 17 T; 0 U; 0 Other;

Gaps ö DB 15; Length 60; ; Score 19.2; DB 15; Length 6; Pred. No. 4.4e+03; 10; Mismatches 23; Indels 22.6%; 41.18; Query Match
Best Local Similarity 41.1%;

ö

GGCTGGGCCCCTCATTTTCGAACTGCGGGTGGCTCCAGTTATCTAGATCCGGTG 56 GGUUAAGGCGUCCCCAAGUUGGAAGGGCGCUUUGCCUUCUGUUUUCUGGAUGCAGAG 26 8 셤

BP ABN53943 standard; DNA; 65 ABN53943; RESULT 8 ABN53943

Mouse spliced transcript detection oligonucleotide SEQ ID NO:26691

(first entry)

15-JUL-2002

mouse; rat; splice transcript; detection; RNA transcript; variant; transcriptome; oligonucleotide library; ss. splice

Mus musculus

WO200210449-A2

07-FEB-2002

20-JUL-2001; 2001WO-IB001903

2000US-0221607P 2001US-0287724P 28-JUL-2000; 02-MAY-2001;

(COMP-) COMPUGEN INC

Faigler S; Mintz L, Mintz E, Shoshan A, Wasserman A,

WPI; 2002-257383/30.

New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of genome, useful for detecting tissue-, pathology-, and developmentalspecific genes

Example 1; SEQ ID NO 26691; 47pp; English.

The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or

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libraries to detect transcripts of a sub-transcriptone under a particular biological or pathological state, and so allowing the detection of tissue - and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect
                                                                                                                                                                                                          developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN5589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
   and in
quantitatively characterising the corresponding transcriptome, and detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini
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Sequence 65 BP; 12 A; 15 C; 19 G; 19 T; 0 U; 0 Other;

Gaps ö 18; Indels DB 6; Length ; Score 19.2; DB 6; ; Pred. No. 4.5e+03; 10; Mismatches 18 22.6%; Query Match Best Local Similarity 41.7% Watches 20; Conservative ò

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72 5 25 UGGUUAAGGCGUCCCCAAGUUGGAAGGCCGCUUUGCUUCUGUUUUCUG 셤

ADM95921/c ID ADM95921 standard; DNA; 80

01-JUL-2004 (first entry)

antisense oligonucleotide #814.

oncogenes; apoptosis related gene, growth factor; chemokine, interleukin; interferon; hormone; neurotransmitter; cell surface antigen; cell adhesion molecule. Rat; antisense oligonucleotide; ss; antisense RNA production; tumour suppressor; cell cycle regulator; ion channel protein; transport protein; intracellular signal transduction; transcription factor; DNA-binding protein; cell-cell communication protein; stress response gene;

Rattus

JS2004072191-A1

15-APR-2004

07-MAR-2003; 2003US-00384245.

07-MAR-2002; 2002US-0362823P.

(CHEN/) CHENCHIK

Chenchik A;

WPI; 2004-373913/35.

gene sequences on nucleic acid arrays, useful for producing a population of distinct antisense RNA molecules from an initial population of distinct mRNA molecules. standardizing control for RNA samples to be tested on non-control Nev

Disclosure; SEQ ID NO 814; 282pp; English.

The invention relates to a standardising control for RNA samples to be tested on non-control gene sequences on nucleic acid arrays, comprising a pool of unique tagged synthetic antisense mRNA molecules of a known concentration, where agequences are unique if their sequences differ. The non-control gene sequences on the nucleic acid array comprise

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channel proteins, transport proteins, intracellular signal transduction modulator and effector factors, transcription factors, DNA-binding proteins, receptors or cell-cell communication proteins, stress response genes, apoptosis related genes DNA synthesis/recombination/repair genes and DNA-binding proteins. The genes encoding receptors comprise receptors for growth factors, chemokines, interleuxins, interferons, hormones, neurotransmitters, cell surface antigens or cell adhesion molecules. The genes encoding cell-cell communication proteins comprise growth factors, chemokines, interferons or hormones. The standardising control for RNA samples to be tested on non-control gene sequences on nucleic acid arrays is useful for producing a population of distinct antisense RNA molecules from an initial population of distinct
                                                                                                                                                                                                                                                                                                                                                                                  mRNA molecules. This sequence represents an antisense oligonucleotide of
suppressors, cell cycle regulators,
                                                                                                                                                                                                                                                                                                                                                                                                                         the invention
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Sequence 80 BP; 21 A; 21 C; 14 G; 24 T; 0 U; 0 Other;

Gaps ö DB 12; Length 80; Indels 72 GCGUCCCCAAGUUGGAAGGGCGCUUUGCUUCUGUUUUCUG 13; 22.6%; Score 19.2; DB 12, 37.5%; Pred. No. 4.8e+03; iive 12; Mismatches 13; Conservative Query Match Best Local Similarity Matches 15; Conserv 52 33 g

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ABZ05513 standard; DNA; 50 RESULT 10 ABZ05513

ABZ05513;

Human leukocyte gene expression profiling probe SEQ ID NO 5504.

(first entry)

09-JAN-2003

17; leukocyte; gene expression profiling; allograft rejection; atherosclerosis; congestive heart failure; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;

Homo sapiens.

WO200257414-A2

25-JUL-2002

22-OCT-2001; 2001WO-US047856

20-OCT-2000; 2000US-0241994P. 08-JUN-2001; 2001US-0296764P.

(BIOC-) BIOCARDIA INC.

Phillips J; Prentice J, Johnson F; Altman P, nuth J, Fry K, Matcuk G, A
Woodward R, Quertermous T, Matcuk G, WPI; 2002-636525/68. Wohlgemuth J, ι, Σ

New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides. Claim 1; Page 506; Opp; English..

The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ0812) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient,

ö i'n prognosis; genetic marker; breast tumor; cytostatic; gynecology and obstetrics; neoplasm; neurodegenerative disease; neuroproposical disease; autoimmune disease; immune discorder; diabetes; antidiabetic; endocrine disease; gastrointestinal disease; metabolic disorder; obesity; genes or markers within each classes is unique to the class relative to the other classes. Also described are: a method of classifying an individual with a condition having good prognosis or poor prognosis; a method of classifying breast cancer patient having good prognosis; a method of assigning individual to several categories in clinical trial; a method of identifying set of genes informative for condition; a method of predicting breast cancer patient with good prognosis or poor prognosis; a microarray; and a microarray kit. The method is useful for identifying informative genes or marker for disease on the phenotypic or genotypic characteristics of the disease condition e.g. cancer, into several classes. A set of genes or marker informative for the condition is identified within each classes, such that the set o predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus, Method of identifying informative genes or marker for breast cancer, involves identifying set of genes or marker informative for condition, each classes such that set of genes in each classes is unique to class relative to other classes. Gaps The invention describes a prognostic method. Samples are classified rheumatoid arthritis, osteoarthritis or cytomegalovirus infection anorectic; nutritional disorder; estrogen receptor negative; ds He Y; . Friend SH, Length 50; Cancer prognosis associated genetic marker SEQ ID NO 140. 15; Indels CCCAAGUUGGAAGGGCGCUUUGCUUCUGUUUUCUGGAUGCAGA 80 2 cercaeracaaaeeeeeerrreeaaererrreeaara Sequence 50 BP; 14 A; 6 C; 17 G; 13 T; 0 U; 0 Other; Score 19; DB 6; 1 Pred. No. 4.9e+03; Stoughton R, Mismatches Disclosure; SEQ ID NO 140; 280pp; English. LICO CO (NECA-) NETHERLANDS CANCER INST. Vant Veer LJ, Lamb J, 10; :: 24-AUG-2004; 2004US-0604076P. 04-FEB-2005; 2005US-0650401P. 07-MAR-2005; 2005WO-US007894. 05-MAR-2004; 2004US-0550810P. (ROSE-) ROSETTA INPHARMATICS 22.4%; 41.9%; AEC75978/c ID AEC75978 standard; DNA; 60 Conservative WPI; 2005-676249/69. Query Match Best Local Similarity Matches 18; Conserv WO2005086891-A2. Homo sapiens. 01-DEC-2005 22-SEP-2005. AEC75978; 38 RESULT 11 និត្តនិត្តនិត្ត ద à

ER/AGE. The cellular constituent profile is used to determine patients suitable for clinical trials of a drug for treating breast cancer and determining if the patient is a good or poor candidate for chemotherapy. The method enables improved and high sensitive prediction of the responsiveness of a breast cancer patient to chemotherapy. The present sequence is a fragment of a human cDNA whose differential expression level makes it a candidate for the cellular constituent profile.

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Gaps

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Score 19; DB 15; Length 60; Pred. No. 5.2e+03; 6; Mismatches 15; Indels

Query Match 22.4%; Best Local Similarity 51.2%; Matches 22; Conservative

Sequence 60 BP; 13 A; 16 C; 15 G; 16 T; 0 U; 0 Other;

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        and obesity. The method provides improved prognostic process to provide appropriate course of prophylaxis and therapy. This sequence represents genetic marker associated with cancer prognosis.
autoimmune, neurodegenerative disorder
                                                                                                                                                                                                                                                                              Diagnosis; prognosis; ss; breast tumor; cancer; cytostatic; neoplasm; DNA microarray; gene expression; tumor marker.
                                                                                               Gaps
                                                                                                                                                                                                                                                          Human cDNA diagnostic/prognostic for breast cancer NM_004207 #2.
                                                                                               ö
                                                                          60;
                                                                      Query Match 22.4%; Score 19; DB 14; Length 60 Best Local Similarity 51.2%; Pred. No. 5.2e+03; Matches 22; Conservative 6; Mismatches 15; Indels
                                                                                                                   43
                                                                                                                               || ::|: || |: || || GITTATTTCCATCTTCCAGGGTGGAAAGAGCTGTCCCCAAG 13
                                                  Sequence 60 BP; 13 A; 16 C; 15 G; 16 T; 0 U; 0 Other;
                                                                                                                  1 GGGUUAUCUGCAACUGAGGGGGGGGGUUAAGGCGUCCCCAAG
such as breast cancer, diabetes,
                                                                                                                                                                                                                                                                                                                                                                                                                       LIC.
                                                                                                                                                                                           AEJ81361 standard; cDNA; 60 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dai H, Friend SH, Deutsch P;
                                                                                                                                                                                                                                                                                                                                                                            06-FEB-2006; 2006WO-US004280.
                                                                                                                                                                                                                                                                                                                                                                                                                      (ROSE-) ROSETTA INPHARMATICS (MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2005; 2005US-0650365P.
                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                    WO2006084272-A2.
                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                     19-0CT-2006
                                                                                                                                                                                                                                                                                                                                                        10-AUG-2006.
                                                                                                                                                                                                                 AEJ81361;
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Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; cytokine; interferon; niterleukin, G-protein coupled receptor; thioesterase; interferon; multifactorial disease; autoimmune disease; infection; nervous system disease; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, Gprotein coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.
43
                      GETITATITICCATCTTCCAGGGTGGAAAGAGCTGTCCCCAAG 13
1 GOGUDAUCUGCAACUGAGGGGGCCUGGUDAAGGCGUCCCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 2462; 4143pp; English
                                                                                                                                                                                                                                                              Human SNP oligonucleotide #3747.
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                                                                                                                                        AAL30539 standard; DNA; 50
                                                                                                                                                                                                                      24-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leach M:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-465210/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200147944-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2001
                                                                                                                                                                               AAL30539;
                                       55
                                                                                                 RESULT 13
                                                                                                                       AAL30539
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Predicting responsiveness of breast cancer patient to chemotherapy based on patient's cellular constituent profile, comprises measurement of cellular constituents, estrogen receptor (ER) level and ER level relative

WPI; 2006-613101/63

Disclosure; SEQ ID NO 140; 349pp; English

to patient's age

The invention relates to predicting responsiveness of a breast cancer patient to chemotherapy, comprising predicting the patient to exhibit enhanced response to chemotherapy as compared to patients in the general population of breast cancer patients if the cellular constituent profile is a poor prognosis profile, and the estrogen receptor (ER) level is ER+ and the ER level relative to patient's age (ER/AGE) is low. Also included are selecting a patient for enrollment in a clinical trial of a drug for treating breast cancer (based on the cellular constituent profile, ER level and an ER/AGE), identifying a breast cancer patient as a good or poor candidate for chemotherapy (based on the cellular constituent profile, ER level and an ER/AGE) and a computer system and program for carrying out the predicting, selecting and identifying methods. In the predicting method, the ER level is determined by methods. In the predicting method, the ER level is determined by encoding the ER is the ERalpha gene. The estrogen receptor level is encoding the ER is the ERalpha gene. The estrogen receptor level is using cyclophosphamide, methotrexate and 5-fluoruracil. The method is useful for predicting responsiveness of a breast cancer patient to chemotherapy based on measurement of cellular constituents, ER level and

Sequence 50 BP; 12 A; 10 C; 20 G; 8 T; 0 U; 0 Other;

organisms

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The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apptocia's related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, Groteins, cytochromes, kinesins, cytokines, interferons, interleukins, Groteins, cytochromes, kinesins, cytokines, interferons, interleukins, Grotein coupled receptors and thioseterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatooid arthritis, multiple sclerosis, diabetes, cystemic lugue erythromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic
                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuroprofective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; collony stimulating factor; complement related protein; cytochome; kinesin; cytokine; interferon; interleukn; G-protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection;
systemic lupus erythromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.
                                                                                                                                                                                                 Gaps
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                                                                                                                                                  Score 18.8; DB 4; Length 50;
Pred. No. 5.9e+03;
3; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                   TGCCACTTACGGGGGCTGGAGGGCCTGGATAAAGACAGAAGGGCG 49
                                                                                                                                                                                                                                           9 uccaacudadagggcuggunaaggcguccccaaguuggaagggcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunosuppressive; immunostimulatory; antiinflammatory;
                                                                                                               Sequence 50 BP; 12 A; 9 C; 21 G; 8 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human SNP oligonucleotide #3746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-DEC-1999; 99US-0173419P.
27-DEC-2000; 2000US-00173419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-DEC-2000; 2000WO-US035498
                                                                                                                                                       th 22.1%;
1 Similarity 56.5%;
26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nervous system disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                 AAL30538 standard; DNA; 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-465210/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200147944-A2.
               systemic lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2001
                                                                                                                                                           Query Match
Best Local S:
Matches 26,
                                                                           organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAL30538;
                                                                                                                                                                                                                                                                                                                                                        RESULT 14
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ID AAL3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents an antisense oligonucleotide of the invention. The antisense oligonucleotide analogs (ONS) have a sequence complementary to a sequence of nucleotides 415-445 of human papilloma virus-16 (HPV-16). The antisense ONS can be used to inhibit expression of HPV gene Es/B7 in living cells, preferably human keratinocytes or human cervical cells. They bind to Es/E7 mRNA in the cell, prevent mRNA translation and promote mRNA degradation by intracellular RNASe H. They can be used for preventing transformation of living cells by HPV. The antisense ONS are used particularly for inhibiting the growth of cervical tumours
                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                               Gaps
                                                                                                                                                                                                                                                                                          HPV-16; inhibitor; antisense oligonucleotide; E6/E7 gene; human;
keratinocyte; cervical cell; cervical tumour; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antisense oligonucleotide analogs for inhibiting growth of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.1%; Score 18.8; DB 2; Length 60; 41.3%; Pred. No. 6.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 DAAGGGGCCCCAAGUUGGAAGGGCGCUUUGCUUCUGUUUUCUGGA 74
 Length 50;
                                                               54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Indels
                               Indels
                                                                                          5 TGCCACTTACGGGGGCTGGAGAGGCCTGGATAAAGACAGAAGGGCG
                                                               9 ugcaacugagagagagugatuaagaggguccccaaguuggaaggggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 60 BP; 14 A; 15 C; 15 G; 0 T; 16 U; 0 Other;
Score 18.8; DB 4;
Pred. No. 5.9e+03;
3; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 7; 40pp; English.
                                                                                                                                                        AAX33875/c
ID AAX33875 standard; RNA; 60 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-US018320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-00929140
                                                                                                                                                                                                                                                                                                                                                         Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alvarez-Salas L;
   Query Match 22.1%;
Best Local Similarity 56.5%;
Matches 26; Conservative
                                                                                                                                                                                                                                     25-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-243727/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                  HPV-16 inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                          WO9913071-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dipaolo J,
                                                                                                                                                                                                                                                                                                                                              Synthetic
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                                                                                                                                                                                                       AAX33875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumors.
                                                                                                                                             RESULT 15
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Search completed: June 19, 2007, 16:30:34

Job time

8 6

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Sequence 2856, Ap
Sequence 2856, Ap
                                                                                                                                       June 19, 2007, 15:46:00 ; Search time 655 Seconds (without alignments) 242.816 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FBMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
/EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
/EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
/EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
/EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
/EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
/EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
/EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
/EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
/EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
/EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
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Sequence
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Sequence
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GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd.
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US-10-131-831-2856
US-09-621-976-13389
US-00-131-837-5504
US-08-291-140-9
US-08-291-140-9
US-08-981-663-59
US-08-981-663-65
US-08-981-663-65
US-08-981-663-65
US-08-981-663-65
US-08-981-663-65
US-08-981-663-65
US-08-109-037-55
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-10-131-827-5504
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                                                                                                                                                                                                                                                                                                                                                                                                                     1403666 seqs, 935554401 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                           OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                             IDENTITY NUC Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                US-10-604-726A-6033
85
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Issued
                                                                                                                                                                                                                                                                   Perfect score:
                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                               Sequence:
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Sequence 2558, Ap Sequence 6041, Ap	6334,	Sequence 2076, Ap	Sequence 6, Appli	Sequence 6, Appli	9	Sequence 6, Appli	9	Sequence 6, Appli	Sequence 6, Appli	Sequence 11, Appl	Sequence 11, Appl	Sequence 12, Appl	Sequence 35, Appl	Sequence 6702, Ap	Sequence 7092, Ap	Sequence 6702, Ap				
US-10-131-831-2558 US-10-131-831-6041	US-10-131-831-6334	US-09-422-978-2076	US-09-121-781-6	US-09-359-193-6	US-09-905-835-6	08-09-896-309-6	US-09-905-847-6	US-09-905-849-6	US-09-905-848-6	NS-09-866-970-6	US-09-895-723-6	US-09-840-459-6	US-09-497-625A-6	US-10-154-515A-11	US-10-122-706-11	US-07-982-712-12	US-09-795-006A-35	US-10-131-827-6702	US-10-131-827-7092	US-10-131-831-6702
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17.8	17.8	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.4	17.4	17.4	17.4
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ALIGNMENTS

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APPLICANT: Wohlgemuth, Jay
APPLICANT: Wohlgemuth, Jay
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Fry, Kirk
APPLICANT: Fry, Kirk
APPLICANT: Fry, Kirk
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
CURRENT APPLICATION NUMBER: US 10/006,290
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: PARENTH NOS: 9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
TITLE OF INVENTION: TRANSPLANT REJECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                 Sequence 2856, Application US/10131827
Patent No. 6905827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2856, Application US/10131831
Patent No. 7026121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA; ORGANISM: Homo sapiens
US-10-131-827-2856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 16; Conserv
                                                                      GENERAL INFORMATION:
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US-10-131-827-2856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 2856
LENGTH: 50
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Sequence 2 Sequence 6 Sequence 6

Sequence

Gaps

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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING TITLE OF INVENTION: TRANSPLANT REJECTION
FILE REPERENCE: 506612000121
CURRENT APPLICATION NUMBER: US/10/131,831
CURRENT FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR PILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9190
SOFTWARE: Patentin version 3.1
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Settle No. 6084090

GENERAL INFORMATION:
APPLICANT: DiPaclo, Joseph
APPLICANT: DiPaclo, Joseph
APPLICANT: BY ANTESENSE LUIS
TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS INHIBITION
TITLE OF INVENTION: BY ANTISENSE OLIGONUCLEOTIDES
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSES: Knobbe, Martens, Olson & Bear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 CCCAAGUUGGAAGGGCGCUUUGCUUCUGUUUUCUGGAUGCAGA
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                                                                                                                                                                                                                                                 Query Match 22.4%; Score 19; DB 3
Best Local Similarity 41.9%; Pred. No. 1e+03
Matches 18; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5504, Application US/10131831
Patent No. 7026121
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SCPTWARE: Patentin version 3.1
; SEQ ID NO 5504
; LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-10-131-827-5504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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US-08-929-140-9/c
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APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
TITLE OF INVENTION: CHRONIC INPLAMMATORY DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 GGGCACCTGCCTAGAGGTAGGGTGGAAACTCCATCCCCAATGAGCACGGGCTCATCTCT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGUUAUCUGCAACUGAGAGGGCUGGUUAAGGCGUCCCCAAGUUGGAAGGGCGCUUUGCU 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.3%; Score 19.8; DB 3; Length 83; 43.7%; Pred. No. 5.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                 Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INPOGNATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Obbert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPERENCE: GENSET: 054PR2;
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT APPLICATION NUMBER: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 13389
LENGTH: 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 AGUUGGAAGGCCCUUUGCUUCUGUUUUCUGGAUGCAGA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 506612000120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-04-04
                                                                                                                                                                                                                                                                                                                                                                              25.2%; Score 21.4; DB 5; 41.0%; Pred. No. 1.2e+02;
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                                CURRENT APPLICATION NUMBER: US/10/131,831
CURRENT FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9190
SOFTWARE: Patentin version 3.1
SEQ ID NO 2856
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PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
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Patent No. 6639063
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Patent No. 6905827
                 FILE REFERENCE: 506612000121
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CORGANISM: Homo sapiens
US-09-621-976-13389
                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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Best Local Similarity
Matches 16; Conserv
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Gaps

Gaps

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Sequence 59, Application US/08981663
Patent No. 5952176
GENERAL INFORMATION:
APPLICANT: MCCARTHY, THOMAS VALENTINE
APPLICANT: GLYCOSYLASE MEDIATED DETECTION OF
TITLE OF INVENTION: GLYCOSYLASE MEDIATED DETECTION OF
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AT CANDIDATE LOCI
                                                                                                                                                                                                                                                                                                                                   Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 UAAGGCGUCCCCAAGUUGGAAGGCGCCUUUGCUUCUGUUUUCUGGA 74
                                                                                                                                                                                                                                                                                                                                                                                                   17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 TACCACGGACCGAAGTCCGTGTGACGCTCTGGTACTGTTCTCTGAA 4
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,663
FILING DATE: 08-JAN-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 descrectricecceccacrácerestráceres de descrectrica de descrectrica de descrectrica de descrectrica de descrectrica de describilita de descr
                                                                                                                                                                                                                                                                                                                               22.1%; Score 18.8; DB 3;
41.3%; Pred. No. 1.3e+03;
tive 10; Mismatches 17;
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Pred. No. 1.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                          TOPOLCGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-560-579A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: SVENSSON, LEONARD R.
REGISTRATION NUMBER: 30,330
REFERENCE DOCKET: 15:31
TELECOMMUNICATION INFORMATION:
                                     SEQUENCE CHARACTERISTICS:
LENGTH: 61 base pairs
                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.9%;
ilarity 51.2%;
Conservative
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 41.3%
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 08
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-981-663-59/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-981-663-59
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1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 DAAGGCGUCCCCAAGUUGGAAGGCCCCUUUGCUUCUGUUUUCUGGA 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Indels
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Patent No. 6277980

GENERAL INFORMATION:
APPLICANT: DiPaolo, Joseph
TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS INHIBITION
BY ANTISENSE OLIGONUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive Sixter
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: NIH138.001A
                                     OPERATING SYSTEM: DOS
SUFTWARE: FastSEQ for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/929,140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Mismatches
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APPLICATION NUMBER: US/09/560,579A
FILING DATE: 28-Apr-2000
CLASSIFICATION: <UNKNOWD>
                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: NIH138.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714/760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/929,140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                   34,115
      IBM Compatible
                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 92660
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 base pairs
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                                                                                                                                                                                            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 19; Conserve
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ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ANTI-SENSE: YES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE
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COUNTRY:
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                                                                                                 GENERAL INFORMATION:
APPLICANT: MCCARTHY, THOMAS VALENTINE
APPLICANT: WALGHAN, PATRICK MARTIN
TITLE OF INVENTION: GLYCOSYLASE MEDIATED DETECTION OF
TITLE OF INVENTION: WUCLEOTIDE SEQUENCES AT CANDIDATE LOCI
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Palls Church
STATE: Virginia
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Patent No. 5952176
GENERAL INFORMATION:
APPLICANT: MCGATHY, THOMAS VALENTINE
APPLICANT: WINGHAN, PATRICK MARTIN
TITLE OF INVENTION: GLYCOSYLASE MEDIATED DETECTION OF
TITLE OF INVENTION: HUCLEOTIDE SEQUENCES AT CANDIDATE LOCI
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STRRET: P.O. Box 747
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18.6; DB 2; Length 76;
Pred. No. 1.7e+03;
6; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,663
FILING DATE: 08-JAN-1998
CLASSIFICATION: 435
ATTORNEY FAGENT INFORMATION:
NAME: SVENSSON, LEONARD R.
RECISTRATION NUMBER: 30,330
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1030 205-8000
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CREANISM: Mycobacterium tuberculosis
US-08-981-663-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                              Sequence 61, Application US/08981663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 21.9%;
Best Local Similarity 51.2%;
Matches 21; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               circular
                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 22040-0747
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                                                                                                                    Patent No. 5952176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Indels
                                             SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,663
FILING DATE: 08-JAN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP STREET: P.O. Box 747 CITY: Falls Church STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 GGGCUGGUUAAGGCGUCCCCAAGUUGGAAGGGCGCUUUGCU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18.6; DB 2;
Pred. No. 1.7e+03;
3; Mismatches 14;
                                                                                                            CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: SVENSSON, LEONARD R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 1377-120P
TELECOMMUNICATION INFORMATION:
TELECHONE: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mycobacterium tuberculosis
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OTHER INFORMATION: /mod_base= i
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.9%;
ilarity 58.5%;
Conservative
                                                                                                                                                                                                                TELERA: (703, LELERA: 248345
INFORMATION FOR SEQ ID NO: 6'
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                 nucleic acid
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                                                                                                                                                                                                                                                                                                                                                   circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 22
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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34 gescrestrresceseceacianaceuseunaseucaseauseu 74
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Pred. No. 1.7e+03;
3; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: James J. Hogan, Diane L. McAllister, APPLICANT: Patricia Gordon, and Philip W. Hammo TITLE OF INVENTION: NUCLEIC ACID PROBES TITLE OF INVENTION: TO UREAPLASMA NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P.C. DOS (Version 3.30)
(Version 5.0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: including application PRIOR APPLICATION DATA: described below: APPLICATION UNBER: 07/879,685 FLING DATE: May 6, 1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PS/2 Model 502 or 55SX
OPRATIG SYSTEM: IBM P.C. DOS (Version 3.3
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
                                                                                                                                                ORGANISM: Mycobacterium tuberculosis FEATURE:
                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: modified_base
LOCATION: 25
OTHER INFORMATION: /mod_base= i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/109,037
                                                                                                                                                                                                NAME/KEY: modified_base
LOCATION: 12
OTHER INFORMATION: /mod_base=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 193/
TELECOMMUNICATION INFRRMATION:
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-109-037-22
; Sequence 22, Application 08/109037
; Patent No. 6093538
                                                TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 21.9%;
Best Local Similarity 58.5%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                NAME/KEY: modified_base
LOCATION: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIPICATION: 436
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
nucleic acid
                                                                                                                                                                                                                                                                                                        LOCATION: 22
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                 YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                              STRANDEDNESS:
                                                                                                               ANTI-SENSE: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90017
                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-981-663-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 66, Application US/08981663
Fatent No. 5952176
GENERAL INFORMATION:
APPLICANT: MCCARTHY, THOMAS VALENTINE
TITLE OF INVENTION: GLYCOSYLASE MEDIATED DETECTION OF
TITLE OF INVENTION: NUCLECTIDE SEQUENCES AT CANDIDATE LOCI
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Flal Church
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18.6; DB 2; Length 76;
Pred. No. 1.7e+03;
6; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCHWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,663
FILING DATE: 08-JAN-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SVENUSSON, LEONARD R.
REGISTATION NUMBER: 30,330
                              PatentIn Release #1.0, Version #1.25 (BPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 GGGCUGGUUAAGGCGUCCCCAAGUUGGAAGGGCGCUUUGCU 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/981,663
FILING DATE: 08-JAN-1998
CLASSIFICATION: 435
ATCHARY/AGENT INFORMATION:
NAME: SVENSSON, LEGNARD R.
REGISTRATION NUMBER: 30,330
REFERNCE/DOCKET NUMBER: 1377-120P
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPERENCE/DOCKET NUMBER: 1377-120P
PELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
        PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 21.9%;
.1 Similarity 51.2%;
21; Conservative
                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 248345
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                 circular
        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Virginia
FRY: USA
22040-0747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
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                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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Gaps

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Length 76; 14; Indels

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APPLICANT: James J. Hogan, Diane L. McAllister,
APPLICANT: Patricia Gordon, and Philip W. Hammond.
TITLE OF INVENTION: NUCLEIC ACID PROBES
TITLE OF INVENTION: TO UREAPLASMA
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: IBM P.C. DOS (Version 3.30) SOFTWARE: WordPerfect (Version 5.0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 436
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 07/879,685
FILING DATE: MAy 6, 1992
ATTONNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
                                                                                                                                                                                                                                                                                          COMPUTER FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage COMPUTER: IBM PS/2 Model 50Z or 55SX
                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/109,037
                                                                                                                                                                   ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Warburg, Richard J
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                               CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                          COUNTRY: U
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                                                                                                ch 21.6%; Score 18.4; DB 3; Length 43; l. Similarity 46.4%; Pred. No. 1.6e+03; 13; Conservative 9; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                           Sequence 55, Application 08/109037

Patent No. 6093538

GENERAL INFORMATION:
APPLICANT: Dames J. Hogan, Diane L. Mcallister,
APPLICANT: Patricia Gordon, and Philip W. Hammond.
TITLE OF INVENTION: NUCLEIC ACID PROBES
TITLE OF INVENTION: TO UREAPLASMA
NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 30017

COMPUTER READABLE FORM:
MEDIUM TYPE: 315" Diskette, 1.44 Mb storage
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: Wordferfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/109,037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 07/879,685
FILING DATE: MAY 6, 1992
ATTORNEY/AGENT INPORMATION:
NAME: Warburg, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                     16 AGAGTGCTTGACTTCTGTGTTCGGGATG 43
                                                                                                                                                                                              49 AGGCGCUUUGCUUCUGUUUUCUGGAUG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 193/121
FELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.6%;
78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 67-3510
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 78.6
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
TOPOLOGY: linear
           STRANDEDNESS: Single
;
TOPOLOGY: linear
US-08-109-037-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 436
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  nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
COUNTRY: USA
                                                                                                         Query Match
Best Local Similarity
Matches 13; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY:
US-08-109-037-55
                                                                                                                                                                                                                                                                                                             RESULT 14
US-08-109-037-55
TYPE:
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32,327

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                                                                               Length 43;
                                                                           Score 18.4; DB 3;
Pred. No. 1.6e+03;
                                                                                                              9; Mismatches
                                                                                                                                              49 AGGGCGCUUUGCUGUUUUCUGGAUG 76
                                                                                                                                                                             28 AGAGTGCTTGACTTCTGTGTTCGGGATG 1
                                                                                                                                                                                                                               Search completed: June 19, 2007, 18:46:09 Job time : 655 secs
                                                                             Query Match 21.6%;
Best Local Similarity 46.4%;
                                                                                                               13; Conservative
nucleic acid
EDNESS: single
            STRANDEDNESS: sir
TOPOLOGY: linear
US-08-109-037-56
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RESULT 15 US-08-109-037-56/c ; Sequence 56, Application 08/109037

Sequence 7115, Ap Sequence 29, Appl Sequence 336, App Sequence 88, Appl Sequence 143, Appl

Sequence 65785,

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APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
FILE REFERENCE: SO6612000120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR PILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: Patentin version 3.1
SEQ ID NO 2856
LENGTH: 50
US-09-908-975-7115

US-09-908-975-29

US-09-908-975-29

US-10-911-838-88

US-10-911-838-84

US-10-911-838-84

US-10-139-900-385-30

US-10-139-900-453865

US-10-179-900-453865

US-10-179-900-453865

US-10-179-900-185-30

US-10-179-900-144-16755

US-10-97-893-22

US-10-97-893-22

US-10-97-893-9639

US-09-908-975-31163

US-09-908-975-31104

US-09-908-975-31104

US-09-908-975-311045

US-09-908-975-24811
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US-10-750-623-13212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 21.4; DB 7;
; Pred. No. 9.9e+02;
12; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2856, Application US/10131827
Publication No. US20040009479A1
GENERAL INFORMATION:
APPLICANT: Wohlgemuth, Jay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.2%;
41.0%;
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11
16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-131-827-2856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS-10-131-827-2856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                            18.2
18.2
18.2
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Best Local
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Sequence 51, Appl
Sequence 26691, A
Sequence 11224, A
Sequence 814, App
Sequence 5504, Ap
Sequence 10113, A
Sequence 4025, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published Applications NA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2856, Ap
Sequence 73, Appl
Sequence 11123, A
                                                                                                                                June 19, 2007, 16:25:24; Search time 744 Seconds (without alignments) 1403.829 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13331,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                 1 ggguuaucugcaacugagag.....uuuucuggaugcagaguccu
      GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-908-975-9052
US-09-908-975-26691
US-09-908-975-26691
US-10-310-914A-11224
US-10-384-245-814
US-10-131-859-53521
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US-10-310-914A-13331
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US-09-908-975-4025
US-10-957-432-458
                                                                                                                                                                                                                                                                                                                                                                          18892170 segs, 6143817638 residues
                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                        nucleic search, using sw model
                                                                                                                                                                                                                                                                                                       IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                US-10-604-726A-6033
85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq length: 0
seq length: 85
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Match
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                                                                                                                                                                                                                                                                                                            Scoring table:
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Sequence 24811, A Sequence 21, Appl Sequence 13212, A Sequence 13212, A

Sequence 92740, A Sequence 110, App Sequence 11045, A 9

Gaps

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US-09-899-575-73/c ; Sequence 73, Application US/0989575 ; Publication No. US20030223961A1 ; GENERAL INFORMATION:

Sequence 11927, A Sequence 6916, Ap Sequence 26823, A

US-10-310-914A-11927 US-10-310-914A-6916 US-11-175-859-26823

Result Š. Length 50;

Sequence 22, Appl Sequence 96333, A Sequence 95334, Ap Sequence 15774, Ap Sequence 3116, Ap Sequence 188, App Sequence 188, App

Searched:

Minimum I Maximum I

Database

Sequence:

Run on:

Sequence 111, App Sequence 166755,

Sequence 22

Sequence 4, Appli Sequence 385230, Sequence 453865, Sequence 172709,

```
APPLICANT: SHOSHAN, Avi
APPLICANT: WASSERWAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: MINTZ, Lat
APPLICANT: PAIGLER, SIMCHON
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                   Length 68;
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Pred. No. 6.7e+03;
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                                                                                                                                                                                                                 Indels
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GENERAL INFORMATION:
FAPPLICANT: Evans, Glen A.
TITLE OF INVENTION: Associated with Bipolar Disorder; TITLE OF INVENTION: Associated with Bipolar Disorder; TITLE OF INVENTION: Associated with Bipolar Disorder; CURRENT APPLICATION NUMBER: 105/09/922,225A; CURRENT FILING DATE: 2003-01-14
NUMBER OF SEQ ID NOS: 117
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 51
LENGTH: 51
                                                                                                                                                                                                                                                                                                             2 eccusaveacuaccueaceceucuecaceacecucccua 42
                                                                                                                                                              Score 20.2; DB 11;
Pred. No. 3e+03;
0; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 20; DB 3;
Pred. No. 3.4e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR FILING DATE: 2000-07-28
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35.3%;
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SOFTWARE: Patentin version 3.0
SEQ ID NO 9052
LENGTH: 60
                                                                                                                                                                   23.8%;
  version 3.3
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US-09-922-225A-51
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US-09-908-975-9052
                                                                                                                                                                   Query Match
Best Local Similarity
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Best Local Similarity
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Best Local Similarity
SOFTWARE: Patentin
SEQ ID NO 13331
LENGTH: 68
                                                                                                , ORGANISM: Human
US-10-310-914A-13331
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                                                                          TYPE: RNA
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Matches
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TITLE OF INVENTION: Bloinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087-0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
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                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: HIV Type C; OTHER INFORMATION: Revexon1 Wild Type
US-09-899-575-73
                                                                       APPLICANT: Van Renaburg, Estrelita Janse
TITLE OF INVENTION: POLYNUCLECTIDES ENCODING ANTIGENIC HIV TYPE C
TITLE OF INVENTION: POLYNEPTIDES, POLYPEPTIDES AND USES THEREOF
TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/899,575
CURRENT APPLICATION NUMBER: 09/475,704
PRIOR PILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 135
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 73
LENGTH: 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 24.5%; Score 20.8; DB 3; 18est Local Similarity 41.1%; Pred. No. 1.8e+03; Matches 23; Conservative 11; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.8%; Score 20.2; DB 1:
68.3%; Pred. No. 2.9e+03
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APPLICANT: Bentwich, Isaac APPLICANT: Shiler, Kvuzat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11123, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin version 3.3
SEQ ID NO 11123
LENGTH: 66
                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                Barnett, Susan W.
Egnelbrecht, Susan
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Best Local Similarity
Matches 28; Conserv
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US-10-310-914A-11123
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US-10-310-914A-13331
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APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR PILING DATE: 2001-10-22
PRIOR PILING DATE: 2000-06
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: Patentin version 3.1
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TITLE OF INVENTION: Method of Analysis of Human Polymorphism FILE REFREENCE: 3690.1
CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 50;
                 Sequence 814, Application US/10384245
Publication No. US20040072191A1
GENERAL INFORMATION:
APPLICANT: Alex Chenchik
TITLE OF INVENTION: Antisense RNA Standardizing Control
FILE REFERENCE: CLON-087PRV
CURRENT APPLICATION NUMBER: US/10/384,245
CURRENT APPLICATION NUMBER: US/10/384,245
NUMBER OF SEQ ID NOS: 1090
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: PASTSEQ for Windows Version 4.0
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7.9e+03;
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Pred. No. 7.9e+C
0; Mismatches
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Publication No. US20060024715A1
GENERAL INFORMATION:
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ilarity 41.9%;
Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wohlgemuth, Jay
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US-10-131-827-5504
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Best Local Similarity
Matches 15; Conserv
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Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Rat
US-10-384-245-814
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LENGTH: 50
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APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Beloinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REPERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PATENTIN VERSION 3.3
                                                                                                                                                                                                                                                                                                               APPLICANT: WASSEMAN, Alon
APPLICANT: WASSEMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: MINTZ, Eli
APPLICANT: MINTZ, Liat
APPLICANT: MINTZ, Liat
APPLICANT: MINTZ, Liat
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REPERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
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  Indels
                                                                              Score 19.2; DB Fred. No. 7.1e+0
                                                50 GGCGCUUUGCUUCUGUUUCUGGAUGCAGAGUC
  13; Mismatches
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PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
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                                                                                                                                                                                                                      Sequence 26691, Application US/09908975
Publication No. US20030165843A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 32337.
SOFTWARE: PatentIn version 3.0
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Best Local Similarity 58.9%;
Matches 33; Conservative
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
CRGANISM: Mus musculus
US-09-908-975-26691
                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS-10-310-914A-11224
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ORGANISM: Human
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LENGTH: 65
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Matches
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Sequence 11927, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: USES thereof
FILE REFERENCE: 06087.0200. CPUSO1
CURRENT APPLICATION NUMBER: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
                                                                                                                                                                                                                                                                                                                 APPLICANT: SADER, WOLFGANG
APPLICANT: HUANG, YING
TITLE OF INVENTION: DETERMINING THE CHEMOSENSITIVITY OF CELLS TO CYTOTOXIC AGENTS
FILE REFERENCE: 2272/04186
CURRENT APPLICATION NUMBER: 2004-10-01
PRIOR APPLICATION NUMBER: 60/508,260
PRIOR PILING DATE: 2003-10-01
NUMBER OF SEQ ID NOS: 758
SOFTWARE: Patentin version 3.3
SEQ ID NO 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18.8; DB 10; Length 70;
Pred. No. 1e+04;
8; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 cueccacacadadedecunicamente de concaudadadaded 47
             Length 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 cugadadedecuedunaadeceuccccaaguusdaagegegeuuug 59
                                                       12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Synthetic polynucleotide sequence US-10-957-432-458
                                                                                                                                                26 TATGTGCAACAAGAGCAGGTGGTTTCCGTGTCTCGAA 63
         Score 18.8; DB 3;
Pred. No. 9.8e+03;
7; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: June 19, 2007, 16:43:03 Job time : 746 secs
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o. US20050208512A1
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63.0%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 45.7%;
Matches 21; Conservative
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             22.1%;
ilarity 50.0%;
Conservative
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Best Local Similarity 63.0
Matches 29; Conservative
         Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                             Sequence 458, Applic Publication No. US20 GENERAL INFORMATION:
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US-10-310-914A-11927
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US-10-957-432-458
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Publication No. US20030165843A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WASSERMAN, Alon
APPLICANT: WINTZ, Eli
APPLICANT: MINTZ, Liat
APPLICANT: THAT POPULATE A TRANSCRIPTOME
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APPLICANT: Banich, Isaac
APPLICANT: Banich, Kvuzat
APPLICANT: Shiler, Kvuzat
TICANT: Shiler, Kvuzat
TITLE OF INVENTION: Uses thereof
FILE REPERENCE: 06087 0200. CPUS01
CURRENT APPLICATION WHOBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 10113
LENGTH: 64
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                                                                                                                                                                                                   Score 19; DB 16;
Pred. No. 7.9e+03;
4; Mismatches 10
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                                                                                                                                                                                                                                                                                            17 AGAGGGCUGGUUAAGGCGUCCCCAAGUUGGAAGG 51
                                                                                                                                                                                                                                                                                                                                   42 AGAGTGGCTGCTAAGGYTCTTCCCAAGTAGGAGGG 8
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CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENC APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: Patentin version 3.0
SEQ ID NO 4025
LENGTH: 65
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Pred. No.
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; Sequence 10113, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
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51.0%;
                  NUMBER OF SEQ ID NOS: 116251
SOFTWARE: Patentin version 3.2
SEQ ID NO 53521
LENGTH: 50
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larity 60.0%;
Conservative
PRIOR FILING DATE: 2004-07-02
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Best Local Similarity 51.0
Matches 26; Conservative
                                                                                                                                  ORGANISM: homo sapien
US-11-175-859-53521
                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 21; Conserv
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US-10-310-914A-10113
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US-09-908-975-4025
                                                                                                               TYPE: DNA
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Sequence Sequence Sequence Sequence

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Scoring table:

Minimum DB seq Maximum DB seq

Database

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Sequence 175427, Application US/10536560

Sequence 175427, Application US/10536560

Sublication No. US200605281A1

GENERAL INFORMATION:

APPLICANT: ROSETTA GENOMICS LTD

TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY

TITLE OF INVENTION: GENES AND USES THEREOF

FILE REFERENCE: 06087.0300. PCU913

FURENT APPLICATION NUMBER: US/10/536,560

CURRENT FILING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 424571

SSOFTWARE: PatentIn version 3.3

SSOFTWARE: PatentIn version 3.3
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US-11-130-645A-575352

US-11-130-645A-518054

US-11-130-645A-618491

US-11-130-645A-618491

US-11-130-645A-618491

US-11-130-645A-103744

US-11-130-645A-103744

US-11-130-645A-10551

US-11-130-645A-10551

US-11-130-645A-10591

US-11-130-645A-10591

US-11-130-645A-418917

US-11-130-645A-418917

US-11-130-645A-418917

US-11-130-645A-418917

US-11-130-645A-97233

US-11-130-645A-97237

US-11-130-645A-97237

US-11-130-645A-97237

US-11-130-645A-97237

US-11-130-645A-9728
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US-11-130-645A-68630
US-11-130-645A-413529
US-11-130-645A-48237
US-11-130-645A-677688
US-11-130-645A-677688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 390712, Application US/10536560. Publication No. US20060257851A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ROSETTA GENOMICS LID
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US-10-536-560-175427
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hes 25; Conserv
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11. | EMC Celerra SIDS3/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
22. | FMC_Celerra SIDS3/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
33. | EMC_Celerra SIDS3/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
44. | EMC_Celerra SIDS3/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
55. | EMC_Celerra SIDS3/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
65. | EMC_Celerra SIDS3/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
77. | EMC_Celerra SIDS3/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
80. | EMC_Celerra SIDS3/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
91. | EMC_Celerra SIDS3/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
92. | EMC_Celerra SIDS3/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
93. | EMC_Celerra SIDS3/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
94. | EMC_Celerra SIDS3/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
95. | EMC_Celerra SIDS3/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
96. | EMC_Celerra SIDS3/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
97. | EMC_Celerra SIDS3/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
98. | EMC_Celerra SIDS3/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
99. | EMC_Celerra SIDS3/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
90. | EMC_Celerra SIDS3/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
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Sequence 2856, Ap
Sequence 2856, Ap
Sequence 423399,
Sequence 543086,
Sequence 54106,
Sequence 31160, A
Sequence 31160,
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                                                                                                                                                                                                               June 19, 2007, 16:28:08 ; Search time 1267 Seconds (without alignments) 692.705 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq
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                                           GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd.
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US-10-536-560-390712

US-10-990-278-2856

US-10-090-288-2856

US-10-006-290-2856

US-10-325-899-2856

US-11-130-645A-423399

US-11-130-645A-57160

US-11-130-645A-31409

US-11-130-645A-31409

US-11-130-645A-31409
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                          nucleic search, using sw model
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85
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length: 85
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Match
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Sequence 609590, Sequence 424753, Sequence 121298, Sequence 456321, Sequence 457656, Sequence 457777, Sequence 97233, A Sequence 97233, A Sequence 31377, Sequence 3594, Ap Sequence 5504, Ap

Sequence 5504, Ap Sequence 68630, A Sequence 413529,

Sequence

Gaps

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211.4 211.4 211.4 20.8 20.8 20.6 20.6 20.6

45967654

Result No.

Gaps

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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING TRANSPLAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Altman, Peter
HITLE OF INVENTION: LEUKOCYTE EXPRESSION PROFILING
                                                                                                                                                                                                                                                                                                                                                                                                                                         42 AGUUGGAAGGGCGCUUUGCUUCUGUUUUCUGGAUGCAGA
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                                                                                                                                                                                                                                                                                                                         25.2%; Score 21.4; DB 7;
illarity 41.0%; Pred. No. 1.7e+03;
Conservative 12; Mismarcher
  PRIOR APPLICATION NUMBER: US 10/121,02.
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2001-10-22
PRIOR PILING DATE: 2001-06-29
PRIOR PILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: Patentin version 3.1
SEQ ID NO 2856
LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 506612000100
CURRENT APPLICATION NUMBER: US/10/006,290
CURRENT FILING DATE: 2001-10-22
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2856, Application US/10006290 Publication No. US20070037144A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wohlgemuth, Jay
APPLICANT: Quertermous, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 8832
SOFTWARE: PatentIn version 3.1
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Phillips, Julie
Woodward, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , ORGANISM: Homo sapiens
US-10-006-290-2856
                                                                                                                                                                                                                                                                            sapiens
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                       ; ORGANISM: Homo US-10-990-298-2856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-325-899-2856
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Publication No. US20070037167A1
GENERAL INFORMATION:
APPLICANT: Woldgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
FILE REFERENCE: 506612000110
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY TITLE OF INVENTION: GENES AND USES THEREOF FILE REPERENCE: 66087.300. PCUS.3 CURRENT APPLICATION NUMBER: US/10/536,560 CURRENT FILING DATE: 2005-05-26 NUMBER OF SEQ ID NOS: 424571 SOFTWARE: Patentin version 3.3 SEQ ID NO 390712 LENGTH: 32
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APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
TITLE OF INVENTION: TRANSPLANT REJECTION
FILE REPERBUECE: 506612000111
CURRENT APPLICATION NUMBER: US.10/990,275
CURRENT FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: US.10/131,831
PRIOR APPLICATION NUMBER: US.10/006,290
PRIOR APPLICATION NUMBER: US.000-6,290
PRIOR APPLICATION NUMBER: US.60/296,764
PRIOR APPLICATION NUMBER: US.60/296,764
PRIOR PILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9190
SOFTWARE: Patentin version 3.1
SEQ ID NO 2856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.2%; Score 21.4; DB 7; 41.0%; Pred. No. 1.7e+03;
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                                                                                                                                                                                                                                                                                                                                                                        13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          57 UNGCUUCUGUUTUCUGGAUGCAGAGUCCU 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 TTGCTTCTGTTTTCTGGATGCAGAGTCCT 4
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CURRENT FILING DATE: 2004-11-15
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55.2%;
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Best Local Similarity 55.2
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-990-275-2856
                                                                                                                                                                                                                             TYPE: RNA
CRGANISM: Homo Sapiens
US-10-536-560-390712
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Best Local Similarity
Matches 16; Conserv
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GENERALL INCRMATION:

GRINGARY AND TEXTURE AMIC, AVNIEL

APPLICANT: Yaal, Asuron

APPLICANT: Yaal, Asuron

APPLICANT: Yaal, Asuron

APPLICANT: Yaal, Asuron

TITLE OF INVENTION: Micrornas and Uses Thereof

FILE REPERENCE: 06087-0202. CPUSI3

FILE REPERENCE: 06087-0202. CPUSI3

CURRENT APPLICATION NUMBER: PCT/US05/1696

PRIOR FILING DATE: 2005-05-14

PRIOR FILING DATE: 2006-05-14

PRIOR FILING DATE: 2006-05-14

PRIOR FILING DATE: 2006-05-14

PRIOR FILING DATE: 2006-03-25

PRIOR FILING DATE: 2006-03-25

PRIOR APPLICATION NUMBER: US 60/665,094

PRIOR FILING DATE: 2005-03-25

PRIOR FILING DATE: 2005-03-25

PRIOR FILING DATE: 2005-03-17

PRIOR FILING DATE: 2005-03-17

PRIOR FILING DATE: 2006-03-17

PRIOR FILING DATE: 2006-03-17

PRIOR FILING DATE: 2006-03-17

PRIOR FILING DATE: 2006-11-15

PRIOR FILING DATE: 2004-11-15

PRIOR PRIOR FILING DATE: 2004-11-15

PRIOR PRIOR FILING DATE: 2004-11-15

PRIOR P
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19 AGGGGCUGGUDAAGGCGUCCCCAAGUUGGAAGGGCGCUUUGCUUCUGUUUUCUGGA
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APPLICANT: Amir, Avniel
APPLICANT: Yael, Karov
APPLICANT: Ranit, Abaronov
TITLE OF INVENTION: Micrornas and Uses Thereof
PILE REFERENCE: 06087.0202.CPUS13
CURRENT APPLICATION NUMBER: US/11/130,645A
CURRENT FILING DATE: 2005-05-16
                                                                                                                                                                                                                                                                 Sequence 543086, Application US/11130645A Publication No. US20070050146A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/USOS/16986
PRIOR FILING DATE: 2005-05-14
PRIOR APPLICATION NUMBER: US 10/709,577
PRIOR FILING DATE: 2004-05-14
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Best Local Similarity 60.73
Matches 34; Conservative
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US-11-130-645A-543086
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Pred. No. 2.9e+03;
0; Mismatches 22; Indels (
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                                                                                                           CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-10-22
PRIOR PILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 9966
SOFTWARE: Patentin Version 3.1
SEQ ID NO 2856
                                           'ERENCE: 506612000122
APPLICATION NUMBER: US/10/325,899
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60.7%;
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       REJECTION
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Best Local Similarity 41.0%
Matches 16; Conservative
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Best Local Similarity 60.7
Matches 34; Conservative
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; ORGANISM: Homo sapiens
US-10-325-899-2856
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; ORGANISM: Homo sapiens
US-11-130-645A-423399
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DB 19; Length 63;

Score 20.6; DB 19. Pred. No. 3.4e+03; 0; Mismatches 14.

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Best Local Similarity 67.4%;
Matches 29; Conservative
; ORGANISM: Homo sapiens
US-11-130-645A-341409
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NUMBER OF SEQ ID NOS: 760616
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Pred. No. 3.4e+03;
0; Mismatches 14; Indels (
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APPLICANT: Yael, Karow
APPLICANT: Ranit, Aharonov
IITLE OF INVENTION: Micrornas and Uses Thereof
FILE REPERENCE: 06087.0202.CPUS13
CURRENT APPLICATION NUMBER: US/11/130,645A
CURRENT FILING DATE: 2005-05-16
                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/666,340
PRIOR FILING DATE: 2005-03-30
PRIOR PELING DATE: 2005-03-30
PRIOR PELING DATE: 2005-03-25
PRIOR PELING DATE: 2005-03-17
PRIOR FILING DATE: 2005-03-17
PRIOR PELING DATE: 2005-03-10
PRIOR PELING DATE: 2005-03-10
PRIOR APPLICATION NUMBER: US 60/593,081
PRIOR PELING DATE: 2005-01-06
PRIOR APPLICATION NUMBER: US 60/522,860
PRIOR PELING DATE: 2004-11-0
PRIOR PELING DATE: 2004-11-16
PRIOR PELING DATE: 2004-11-10
PRIOR APPLICATION NUMBER: US 60/522,457
PRIOR PELING DATE: 2004-11-10
PRIOR DATE: 2004-11-10
PRIOR PELING DATE: 2004-11-10
PRIOR DATE: 2004-11-10
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PRIOR PELLING DATE: 2005-05-14
PRIOR PELLING DATE: 2005-05-14
PRIOR PELLING DATE: 2005-05-14
PRIOR FILING DATE: 2004-05-14
PRIOR FILING DATE: 2004-05-14
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PRIOR PELLING DATE: 2005-03-25
PRIOR PELLING DATE: 2005-03-17
PRIOR PELLING DATE: 2005-03-16
PRIOR PELLING DATE: 2005-01-06
PRIOR PELLING DATE: 2005-01-06
PRIOR PELLING DATE: 2005-10-06
PRIOR PELLING DATE: 2005-11-06
PRIOR PELLING DATE: 2004-12-08
PRIOR PELLING DATE: 2004-11-15
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Publication No. US20070050146A1
GENERAL INFORMATION:
              US 10/709,572
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Best Local Similarity 67.4%;
Matches 29; Conservative (
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US-11-130-645A-57160
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LENGTH: 63
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PRIOR APPLICATION NUMBER: US 10/709,577
PRIOR FILING DATE: 2004-05-14
PRIOR PLING DATE: 2004-05-14
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PRIOR APPLICATION NUMBER: US 60/666,340
PRIOR FILING DATE: 2005-03-30
PRIOR FILING DATE: 2005-03-25
PRIOR PLING DATE: 2005-03-25
PRIOR APPLICATION NUMBER: US 60/662,742
PRIOR PLING DATE: 2005-03-17
PRIOR PLING DATE: 2005-03-17
PRIOR PLING DATE: 2005-01-06
PRIOR PLING DATE: 2004-11-06
PRIOR PLING DATE: 2004-11-06
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Pred. No. 4.7e+03;
0; Mismatches 8;
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TITLE OF INVENTION: Micrornas and Uses Thereof
FILE REFERENCE: 06087,0202.CPUS13
CURRENT APPLICATION NUMBER: US/11/130,645A
CURRENT FILING DATE: 2005-05-16
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Sequence 175103, Application US/11130645A Publication No. US20070050146A1
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PRIOR FILING DATE: 2005-05-14
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SEQ ID NO 175103
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Best Local Similarity 75.8%;
Matches 25; Conservative
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Yael, Karov
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US-11-130-645A-175103
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              Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 760616
SOFTWARE: Patentin version 3.3
SEQ ID NO 518054
LENGTH: 64
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SEQ ID NOS: 760616
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4.7e+03;
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TITLE OF INVENTION: Micrornas and Uses Thereof
FILE REFERENCE: 06087.0202.CPUS13
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Pred. No. 4.7e+
0; Mismatches
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Pred. No. 4.7e+
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PRIOR FILING DATE: 2005-05-14
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PRIOR APPLICATION NUMBER: US 60/665,094
PRIOR FILING DATE: 2005-03-25
PRIOR APPLICATION NUMBER: US 60/662,742
PRIOR APPLICATION NUMBER: US 60/593,329
PRIOR PILING DATE: 2005-03-17
PRIOR PILING DATE: 2005-01-06
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PRIOR APPLICATION NUMBER: US 60/522,457
PRIOR FILING DATE: 2004-10-04
Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 760616
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CATION NUMBER: US 10/709,572
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PRIOR APPLICATION NUMBER: US 60/666,340
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PRIOR FILING DATE: 2004-12-08
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PRIOR APPLICATION NUMBER: US 60/522,860
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75.8%;
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59.6%;
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PRIOR FILING DATE: 2004-10-04
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Best Local Similarity 59.8.
...hes 34; Conservative
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Yael, Karov
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CORGANISM: Homo sapiens
US-11-130-645A-520800
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US-11-130-645A-518054
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US-11-130-645A-618491
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SEQ ID NO 520800
LENGTH: 64
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Matches 25
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 275352
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Pred. No. 4.7e+03;
0; Mismatches 8;
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FILE REFERENCE: 06087.0202.CPUS13
CURRENT APPLICATION NUMBER: US/11/130,645A
CURRENT FILING DATE: 2005-05-16
PRIOR APPLICATION NUMBER: PCT/US05/16986
                                      ATION NUMBER: US/11/130,645A
                                                                                           APPLICATION NUMBER: PCT/USOS/16986
FILING DATE: 2005-05-14
APPLICATION NUMBER: US 10/709,577
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                                                                                                                                                                                                                                                                     FILING DATE: 2004-05-14
APPLICATION NUMBER: US 60/666,340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2005-03-17
APPLICATION NUMBER: US 60/593,329
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APPLICATION NUMBER: US 60/522,860
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APPLICATION NUMBER: US 10/709,577
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APPLICATION NUMBER: US 10/709,572
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                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2005-03-30
APPLICATION NUMBER: US 60/665,094
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APPLICATION NUMBER: US 60/593,081
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APPLICATION NUMBER: US 60/522,457
FILING DATE: 2004-10-04
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APPLICATION NUMBER: US 60/522,860
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APPLICATION NUMBER: US 60/522,457
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REFERENCE: 06087.0202.CPUS13
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APPLICATION NUMBER: US 1
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Best Local Similarity 75.8%;
Matches 25; Conservative
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Yael, Karov
Ranit, Aharonov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-130-645A-275352
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Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 76616

SOFTWARE: PatentIn version 3.3

SEQ ID NO 618491

LENGTH: 64

TYPE: RNA

ORGANISM: Homo sapiens

US-11-130-645A-618491
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                                           GENERAL IN. CALLANDER ADDITONATE APPLICANT: Bentwich, Itzing.

APPLICANT: Amir, Avniel
APPLICANT: Yael, Karov
APPLICANT: Yael, Karov
APPLICANT: Ranit, Aharonov
APPLICANT: Pael, Karov
APPLICANT: Wael, Karov
APPLICANT: Wall Anaronas and Uses Thereof
FILE REFERENCE: 06087.0202.CPUS13
CURRENT APPLICATION NUMBER: US/11/130,645A
CURRENT APPLICATION NUMBER: US/11/130,645A
FRIOR FILING DATE: 2005-05-16
PRIOR PELING DATE: 2005-05-14
PRIOR PELING DATE: 2006-05-14
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PRIOR PLING DATE: 2005-03-17
PRIOR APPLICATION NUMBER: US 60/655,094
PRIOR PLING DATE: 2005-03-17
PRIOR APPLICATION NUMBER: US 60/523,081
PRIOR PILING DATE: 2005-01-06
PRIOR APPLICATION NUMBER: US 60/522,860
PRIOR APPLICATION NUMBER: US 60/522,860
PRIOR APPLICATION NUMBER: US 60/522,860
PRIOR APPLICATION NUMBER: US 60/522,457
PRIOR PRIOR PRIUG DATE: 2004-112-08
PRIOR APPLICATION NUMBER: US 60/522,457
Publication No. US20070050146A1
GENERAL INFORMATION:
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Best Local Similarity 75.8
Matches 25, Conservative
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Gaps

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Search completed: June 19, 2007, 18:08:19 Job time : 1268 secs

9 22.4 65 16 BZ592639 9 22.4 70 14 CX296360 9 22.4 74 17 CG646686 9 22.4 81 15 BH416654 8 22.1 69 10 CV294687	8 22.1 73 15 AZ784729 8 22.1 75 19 CR161283 8 22.1 84 2 BF531086 8 22.1 84 19 BX003952 6 21.9 44 2 BF102281	18.6 21.9 61 15 AZ918852 AZ918852 1006011E1 18.6 21.9 63 7 AU255617 AU25577 AU255617 AU25577 AU25577	4 .21.6 50 16 BH861963 4 .21.6 65 10 CT685647 4 .21.6 71 12 EB421640 4 .21.6 76 11 BC732719	4 21.6 78 9 CK125805 4 21.6 81 5 CA833496	21.6 84 3 B1828236 4 21.6 84 3 B1828236 21.6 84 12 BB423837	2 21.4 63 10 CV583912 2 21.4 81 15 AZ386677 2 21.4 83 8 CR453329	2 21.4 84 3 3 21.2 50 7 8 21.2 67 15	ALIGNMENTS	EC651791 81 bp mRNA linear EST 29-JUN-2006	CDNA, mRNA sequence. EC651791 EC651791.1 GI:109759395	EST Cya Cya		Cyanophora paradoxa [Durnford lab] Unpublished (2006) Contact: TBestDB			/organism="Cyanopi /mol_type="mRNA" /Mb xrefe"texon:27 /Clone llb="Cyanopi /note="Durnford la	atch 25.6%; Score 21.8; DB 11; Length 81; 20; Conservative 12; Mismatches 17; Indels 0; Gaps 0; 23 GCUGGUDAAGGCGCCCCAAGUUGCAAGGCGCUUUGCUUCUUUUU 71 : :: :: ::
C 15 17 17 C 19 C 19		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 C C C C C C C C C C C C C C C C C C C	ት ነገር የ	00		2 4 4 2 4 4 3 4 5		RESULT 1 EC651791 LOCUS	ACCESSION	KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	JOURNAL		FEATURES	POLIGIN	Query Match Best Local S Matches 20 Qy 23
6.2.1 Biocceleration Ltd.	:1 Search time 4740 Seconds (without alignments) [112.550 Million cell updates/sec	5	residues	rs: 709684									ted by chance to have a of the result being printed, core distribution.		Description	EC651791 CDE000093 BX947927 Arabidops DX796917 PMAL-aaa5 AV858990 AV858990 DN496062 P034A09.5 EB92723 12064370	Forward Mus muscu S05505 F Pan trog v160c6.8 v160202AP cf18b11.xA
GenCore version pyright (c) 1993 - 2007	nucleic search, using sw model June 19, 2007, 15:45:58 ; Searc (wit	4-726A-6033 ucugcaacugagag	IDENTITY NUC Gapop 10.0 , Gapext 1.0 53585215 segs, 31020513797 resi	hits satisfying chosen parameters	length: 0 length: 85	<pre>j: Minimum Match 0% Maximum Match 100% Listing first 45 summaries</pre>	EST:* : gb_est1:* : gb_est3:*	gb_est4:* gb_est5:* qb_est6:*	6: gb_htc:* 7: gb_est2:* 8: gb_est7:* 9: gb_est8:* 10: cb_est8:*	: gb_est13:* : gb_est12:* : gb_est11:*	: gb_est10:* : gb_gss1:* : gb_gss2:* : qb_gss3:*	. gb_gss4:* . gb_gss5:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being pri and is derived by analysis of the total score distribution.	SUMMARIES	Query Match Length DB ID	25.6 81 11 BC651791 24.9 64 19 BX947927 24.0 77 AV958990 23.8 82 13 DN496062 23.5 81 12 BB27323 24.7 7 AV958990	668 14 6 7 7 9 10 9 7 9 10 9 10 9 10 9 10 9 10 9

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Wilson, R.
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Direct Submission

Submitted (31-MRA-2004) Weisshaar B., Max-Planck-Institut fuer

Submitted (31-MRA-2004) Weisshaar B., Max-Planck-Institut fuer

Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence has been recovered from the left border of the T-DNA.

It indicates an insertion close to or within gene At3916050.

Details on the protocols used for generation of the sequence are
described in References 1-3. The sequences are generated at the MPI
for Plant Breeding Research in the context of the GABI-Kat project.

GABI-Kat is part of the German Plant Genomics program designated

'GABI'. Information on line availability can be found at:

Location/Qualifiers
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/note="PCR was performed on DNA from Arabidopsis thaliana plants (TI) which were transformed with the T-DNA from vector pAcifol (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment (s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Weisshaar, B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
                                                  BX947927 64 bp DNA linear GSS 05-APR-2004
Arabidopsis thaliana T-DNA flanking sequence GK-785G09-024929,
                                                                                                                                                                                                                        Arabidopsis thaliana
Stakaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
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mol type="genomic DNA"
dD_xref="taxon:3702"
clone="GK-785G09-024929"
                                                                                                                                                                                                                                                                                                                                                                                                                                             Bioinformatics 19 (11), 1441-1442 (2003)
12874060
                                                                                                                                                                                                   Arabidopsis thaliana (thale cress)
                                                                                                        genomic survey sequence.
                                                                                                                                                     BX947927.1 GI:42597613
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     RESULT 2
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AV858990 Nori Satoh unpublished cDNA library, larva Ciona intestinalis cDNA clone rcilv21013 3', mRNA sequence.
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DY796917 13 bp mRNA linear EST 21-MAR-2006
PMAL-aaa57205.b1 Lamprey_EST_Tissues Petromyzon marinus.cDNA 3',
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1 (Dases I to 77)
Satch, N., Satou, Y., Kohara, Y. and Shin-i, T.
Expressed genes in Ciona intestinalis
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: submissions@watson.wustl.edu
Library material provided by Department of Fisheries & Wildlife,
Michigan State University Library constructed by Ziping Zhang;
Yilei Wang; Weiming Li Library sequenced by Washington University
Genome Sequencing Center
                                                                                                                                                          bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
11 (bases 1 to 73)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="Adult"
/lab_host="DH10B"
/clone_lib="Lamprey_EST_Tissues"
/note="Vector: pDNR-LIB; Site_1: Sfi I; Site_2: Sfi I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                   Contact: Ziping Zhang
WashU Lamprey EST project
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Petromyzon marinus"
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Best Local Similarity 40.5%; Pred. No. 4.2e
                                                                                                                                                  Petromyzon marinus (sea lamprey)
Petromyzon marinus
Eukaryota; Metazoa; Chordata; Cri
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/db_xref="taxon:7757"
/sex="Mix"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: pDNR-LIB-reverse.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                WashU Lamprey EST project
Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AV858990.1 GI:16846514
                                                                                                          DY796917.1 GI:90141134
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Department of Zoology
Kyoto University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ciona intestinalis
Ciona intestinalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
                                                          mRNA sequence.
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AUTHORS
TITLE
JOURNAL
COMMENT
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Gaps

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36 UCCCCAAGUUGGAAGGCCCUUUGCUUCUGUUUUCUGGAUGC 77

Length 64;

24.9%; Score 21.2; DB 19; 40.5%; Pred. No. 3.5e+04; tive 12; Mismatches 13;

17; Conservative

Best Local Similarity Matches 17; Conserv

ð d

Query Match

82 AGGAGGAGGAGGTTTCTTCAACTCTCACCGGCATTATCTTTTCTGTTTTATGTAT 26

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REFERENCE
                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                RESULT 6
EB927323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DN496062 82 bp mRNA linear EST 10-MAR-2005 P034A09.5pR Populus petioles cDNA library Populus tremula cDNA clone P034A09 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Populus tremula

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids I; Malpighiales; Salicaeae; Saliceae; Populus.

1 (bases 1 to 82)

Sterky,Fr. Bhalerao,R.P., Unneberg,P., Segerman,B., Nilsson,P.,

Strause; S.H., Sundberg,B., Gustafsson,P., Unlen,M., Bhalerao,R.P.,

Nilsson,O., Sandberg,G., Karlsson,P., Unlen,M., Bhalerao,R.P.,

A Populus EST resource for plant functional genomics

Proc. Natl. Acad. Sci. U.S.A. 101 (38), 13951-13956 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                             7 UCUGCAACUGAGAGGGGCUGGUUAAGGCGUCCCCCAAGUUGGAAGGGCGCUUUGCUUCUGU 66
                                                                                                                                                                                                           /tissue type="whole animal"
/dev_stage="larva"
/clone_lib="Nori Satoh unpublished cDNA library, larva"
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Umea Plant Science Center, Department of Plant Physiology
Umea University
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/clone_lib="Populus petioles cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.8%; Score 20.2; DB 13; Length ilarity 36.8%; Pred. No. 7.9e+04; Conservative 13; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                             26; Indels
                                                                                                                                                                                                                                                                                                                24.0%; Score 20.4; DB 7; 37.1%; Pred. No. 6.7e+04; iive 13; Mismatches 26;
                                                           Email: satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
                                                                                                                              /organism="Ciona intestinalis"
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Pax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: bo.segerman@plantphys.umu.se.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Populus tremula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:113636"
/clone="P034A09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Other ESTs: P034A09, P034A09.3pR
Contact: Bo Segerman
                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:7719"
/clone="rcilv21o13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DN496062.1 GI:60706252
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Best Local Similarity
Matches 23; Conserva
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Best Local Similarity
Matches 21; Conserv
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TT 13
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DN496062/c
LOCUS
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19 AGGGGCUGGUUAAGGCGUCCCCAAGUUGGAAGGGCGCUUUGCUUCUGUUUUCUGGAU 75

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EST 25-MAY-2006
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Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,
Jonkers, J., Smith, P., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,
Rogers, J. and Bradley, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CR024485 16 DNA linear GSS 05-JUL-200 Forward strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHPP304604, genomic survey sequence.
                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
                                                                                                                                                                                                                                                      Chen, F., Jin, Y., Zeng, K., Gnirke, A., Baille, M., Cheung, L.M., Chong, A., Garrick, B., Murray, L., Oliva, J., Park, C., Reyes, J., Tang, J., Amundsen, C., Orton, A., Shao, A., Platt, D. and Swimmer, C. Exelixis Danio rerio EST project Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rogers, J. and Bradley, A.
Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CBIO 1SA, UK. http://www.sanger.ac.uk/MICER
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
H927323 81 bp mRNA linear EST 25-N
2064370 2F31 Danio rerio cDNA clone 3269876, mRNA sequence.
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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 UGGUUAAGGCGUCCCCAAGUUGGAAGGCCGCUTUGCUUCUGUTUUCU 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="ZF31"
/note="Vector: pSPORT-1; dT primed cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                  Open Biosystems, Inc.
6705 Odyssey Drive, Huntsville, AL 35806, USA
Email: KSCHMITT@OPENBIOSYSTEMS.COM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 23.5%; Score 20; DB 12;
Best Local Similarity 31.9%; Pred. No. 9.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CR024485
CR024485.1 GI:49757540
GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                     Actinopterygii, Neopterygii, Telec
Cypriniformes, Cyprinidae, Danio.
1 (bases 1 to 81)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .76
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .81
/organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPP304d04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:7955"
/clone="3269876"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="testis"
/lab_host="DH12s"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                      EB927323.1 GI:101629537
                                                                                                                 Danio rerio (zebrafish)
                                                                                                                                                                                                                                                                                                                                                                            Contact: Karin Schmitt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                            Danio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                   DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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KEYWORDS
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AUTHORS
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JOURNAL
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Gaps

ö 67 81

63

셤 8 셤 VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

ACCESSION

LOCUS

AK197638 RESULT 8

Query Match Best Local

ORIGIN

Matches

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DQ041030 68 bp DNA linear GSS 02-JUN-2005
Pan troglodytes HC7216 gene, VIRTUAL TRANSCRIPT, partial sequence,
                                                                                                                                                                                                                                                         BU865564 84 bp mRNA linear EST 16-OCT-2002 S055D05 Populus imbibed seed cDNA library Populus tremula cDNA 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
The poplar tree transcriptome: Analysis of expressed sequence tags
from multiple libraries
Unpublished (2002)
Contact: BHALERAO RUPALI R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
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Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
|db_xref="taxon:113636"
|/tissue_type="imbibed_seed"
|clone_lib="Populus imbibed_seed_cDNA_library"
                                                                      18 GAGGGGCUGGUDAAGGCGUCCCCAAGUUGGAAGGGCGCUUUGCUUCUGUU
                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
Pred. No. 1.2e+05;
6; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.1%; Score 19.6; DB 4; 42.3%; Pred. No. 1.2e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
121: +46 90 786 5278
Fax: +46 90 786 6676
Email: rupali.bhaleraooplantphys.umu.se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Populus tremula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Mismatches
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15869325
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Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                 BU865564.1 GI:24056218
                                                                                                                                                                                                                                                                                                          prime, mRNA sequence.
BU865564
  50.08;
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  Best Local Similarity 50.0
Matches 25, Conservative
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Best Local Similarity
Matches 11; Conserv
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                           25;
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DQ041030/c
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Hori, F., Imotani, K., Kawai, J., Kondo, S., Murata, M., Nakamura, M.,
Nomura, K., Ohno, M., Sasaki, D., Shiraki, T., Waki, K., Watahiki, A. and
Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (15-5EP-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Parghoration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alternative Splicing Libraries (ASLs) are prepared by: Preparating of single-stranded DNA using a RNA template from full length CDNA libraries, hybridizating of semoing single-stranded DNAs, removing of remaining single-stranded DNA, digesting of regions comprising double-stranded DNA by a set of bp-cutters, capturing of DNA hybrids with loop structures (alternative spliced exon), ligating of Y-shaped primers to isolated DNA hybrids with loop structures to isolated DNA hybrids with loop structures to ligation products and their cloning into pFLCI vector. (Reference). Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Watahiki, A., Waki, K., Hayatsu, N., Shiraki, T., Kondo, S.,
Nakamura, M., Sasaki, D., Arakawa, T., Kawai, J., Harbers, M.,
Hayashizaki, Y. and Carninci, P.
Libraries enriched for alternatively spliced exons reveal splicing
patterns in melanocytes and melanomas
Nat. Methods 1 (3), 233-239 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AK197638 HTC 23-NOV-200
Mus musculus CDNA, clone:Y1G0125L04, strand:minus,
reference:ENSEMBL:Mouse-Transcript-ENST:ENSMUST00000045844, based
                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                             GUNAUCUGCAACUGAGGGGCUGGUNAAGGCGUCCCCAAGUUGGAAGGCGCCUUUGCUU
                                                                                                               Gaps
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                                                      Length 76;
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Fax:81-45-503-9216)
                                                                                                            32; Indels
                                                         23.3%; Score 19.8; DB 19; 36.6%; Pred. No. 1.1e+05; cive 13; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'organism="Mus musculus"
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HTC; ASSETS.
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Mus musculus CDNA,
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                                                                                                            Conservative
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61 ATGTTTACTTG 71
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                                                                                    Similarity
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TITLE JOURNAL

COMMENT

REFERENCE AUTHORS

JOURNAL PUBMED

TITLE

source

ORIGIN

FEATURES

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84;

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Query Match 22.8%;
Best Local Similarity 53.3%;
Matches 24; Conservative 5
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Best Local Similarity 48.9%;
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A1423081.1
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Glires; Rodentia;
Marmalia; Butheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus

1 (bases 1 to 79)
Martra M., Hillier, L., Allen, M., E., Mowles, M., Dit, Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moorre, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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79 bp mRNA linear EST 09-OCT-1997 v16006.81 Knowles Solter mouse 2 cell Mus musculus cDNA clone IMAGE:976618 5' similar to gb:X53741_rnal FIBULIN-1, ISOFORM A PRECURSOR (HUMAN); mRNA sequence.
      Sackton, T.B.,
Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B. Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civello, D., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLML ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="embryo"
/dev_stage="2-cell"
/lab_host="labor"
/clone_lib="Knowles Solter mouse 2 cell"
/note="Organ: embryo; Vector: pBluescribe (modified);
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                    Score 19.4; DB 19; Length 68; Pred. No. 1.4e+05; 3; Mismatches 11; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 AGCCAGGCGGGTAAATGCGTCCCAGCGTAGGGAGGGC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 AGAGGGCUGGUUAAGGCGUCCCCAAGUUGGAAGGGC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/strain="C57BL/6J x DBA/2J Fl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trace considered overall poor quality

    .68
    /organism="Pan troglodytes"

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Contact: Marra M/Mouse EST Project
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/db_xref="taxon:9598"
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/clone="IMAGE:976618"
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AA619735.1 GI:2523611
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Matches 23; Conserv
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      AUTHORS
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A1423081 ST 28-WAR-1999 tf18b11.x1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:2096541 3' similar to TR:Q15214 Q15214 SALIVARY PROLINE-RICH PROTEIN 1 ;, mRNA
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CNB69173 85 bp mRNA linear EST 03-JUN-2000 001202AAOA004538HT (AAOA) Royal Gala phloem Malus x domestica CDNA clone AAOA004538, mRNA sequence.
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1 (bases 1 to 85)
Beuning,L., Bowen,J., Crowhurst,R., Gleave,A., Janssen,B., McArtney,S., Newcomb,R., Ross,G., Snowden,K., Walton,E. and Yauk,Y. Unpublished (2004)
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/note="Vector: pBluescript SK(-); Library sequenced 
Genesis Research & Development"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Gleave, A.
Sequencing Facility
The Horticulture and Food Research Institute of New Zealand
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
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                                                                                                                                                                                                                                                                                                                 17 AGAGGGGCUGGUUAAGGCGUCCCCAAGUUGGAAGGGCGCCUUUGCU 61
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                                                                                                                                                                                                                                                                  16; Indels
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Pred. No. 1.5e+05;
5; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                              29 AGAGGAGGTGAAAGCACAAGCAAGTTAGATGAAGAAGTTGCT
                                                                                                                                                                                                           Score 19.4; DB 1;
Pred. No. 1.4e+05;
7; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Malus x domestica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:3750"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@hortresearch.co.nz.
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith,
                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strain="Czech II"
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BZ592639/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T 3/1; double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BI408546 55 bp mRNA linear EST 14-AUG-2001
602963185F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5118812 5',
                                                                                                                                                                                                                                                                                                                                                                        Bonaldo, Ph.D. cDN Arrayed by: Greg Lennon, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. CDNA Library Arrayed by: Washington University Genome Sequencing by: Washington University Genome Sequencing Center Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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/clone lib="NCI CGAP Brn23"
/note="Cogan: brain; Vector: pT7T3D-PacI; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 55)
11 (harte; //mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Haplorrhin;
                                                                                             Catarrhin; Hominidae; Homo.

(Dases 1 to 58)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAIJONAL CAGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAIJONAL CAGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP-PEGAP); Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.6%; Score 19.2; DB 1; Length 58; 35.4%; Pred. No. 1.6e+05; tive 13; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 GCCCCCCTTGTGTTTTTTTTTTTCCCCTGCCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'tissue_type="glioblastoma (pooled)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trace considered overall poor quality Insert Length: 2477 Std Error: 0.00 Seq primer: -40VP from Gibco High quality sequence stop: 1. Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:2096541"
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           Homo sapiens (human)
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Best Local Similarity 35.4%
Marches 17; Conservative
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Bonaldo, Ph.D. constraint of the I.M.A.G.E. Consortium (LLNL) constituted by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://mage.llnl.gov constitution in column: 21
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lines
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Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kin,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library went through one round of normalization, and was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue type="pooled lung tumors"
/lab_host="DH10B (phage-resistant)"
/clone lib="NCI_CGAP_Lul3"
/note="Organ: lung, Vector: pT7T3D-Pac1; Site_1: NotI;
Site_2: EcoR1; lst strand cDNA was prepared from mRNA
obtained from pooled lung tumors with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 bp DNA. linear GSS 07-JAN-2
SALK 028210 16.80.n Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_028210.16.80.n, genomic
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                   cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 GAGGGGUGGUUAAGGCGUCCCCAAGUUGGAAGGG 52
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                                                                                                                                                                                                                                                                                                                                                                  1. .55
/organism="Mus musculus"
                                                                                                                                                                                                                                                                        High quality sequence start: 11
High quality sequence stop: 46.
Location/Qualifiers
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/clone="IMAGE:5118812"
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TDNA. This sequence lies within an annotated exon of At5g65210.
Class: TDNA tagged.
Location/Qualifiers
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Best Local Similarity 50.0%; Pred. No. 1.9e+05;
Matches 18; Conservative 7; Mismatches 11; Indels
                                                          /organism="Arabidopsis thaliana"
|mol_type="genomic DNA"
|-coctype="Col-0"
|db_xref="taxon:3702"
                              FEATURES
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Search completed: June 19, 2007, 17:47:05 Job time: 4746 secs

4 UNAUCUGCAACUGAGGGGGCGCGCGCCC 39

Rattus no

Sequence Sequence

Sequence

Sequence

Antisense

Synthetic

Sequence

Minimum DB Maximum DB

Database

Result 8

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Searched:

OM nucleic

Run on:

Sequence:

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AR240243
AR150043
BD27816
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BD31800
AR2313914
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                                                                                                                                                                                                                                                                                                                                                                                                                                           1.24
/organism="synthetic construct'
/mol type="unassigned DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                               DNA
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Probes and decoder oligonucleotides
Patent: WO 0216649-A 365 28-FEB-2002;
Illumina, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                            other sequences; artificial sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 bp Dl Sequence 4341 from Patent WO0216649. AX447886.1 GI:21696785
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Sequence 365 from Patent WO0216649.
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AX298773
AR069252
CS102090
CS102090
DQ755439
AR240243
AR150048
BD27916
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BD27916
BD27918
BD279180
BD313314
AR41243
AR44243
AR4404657
BD271506
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AR41807
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AR036420 Sequence
129861 Sequence
122320 Sequence
162210 Sequence
16230 Sequence
180379515 Method an
BD379516 Method an
BD379518 Method an
AX215297 Sequence
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                                                          June 19, 2007, 12:41:00 ; Search time 1106 Seconds (without alignments) 1499.898 Million cell updates/sec
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BD405918 G
        GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd
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                                                                                                                                                                 7568541 segs, 34560148153 residues
                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                     1 ugagagggcugguuaaggcgucc 24
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                                             nucleic search, using sw model
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BD379515
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Perfect score:
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Gaps

REFERENCE AUTHORS TITLE

JOURNAL

PEATURES

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FAG19, disigned sense primer based on 11 between 1464 and 1484
Key
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                                                              Fagan, R.J., Phelps, C.B., Phillips, T., Pierron, V.N., Allen, K.E., Allen, J.M. and Potter, S.J.
Nuclear hormone receptor ligand binding domain
Patent: WO 02070557-A 6 12-SEP-2002;
Inpharmatica Limited (GB)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 21;
                                                                                                                                                                                                                                                                                                                     Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suzuki, E., Miyatake, K. and Hayakawa, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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68.8%; Pred. No. 3.2e+05;
iive 4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                 Score 14.6; DB 2;
Pred. No. 2.5e+05;
4; Mismatches 4;

    21
    Organism="synthetic construct"
|mol type="unassigned DNA"
|db_xref="taxon:32630"

    .24
        /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"</pr>

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamakawa, H., Suzuki, E., Miyatake, K. and Method of food analysis Patent: w0 03068964-A 7 21-AUG-2003; H YAMAKAWA et al. OS Artificial Sequence PN W0 03068964-A/7 PD 21-AUG-2003 PF 26-SEP-2002 WO 2002JP009982 PR 15-FSB-2002 JP 02P 038930 PR 15-FSB-2002 JP 02P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           other sequences; artificial sequences.
1 (bases 1 to 21)
                                 other sequences; artificial sequences.
                                                                                                                                                                                                                                                               'note="LBDG3 Reverse primer"
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Sequence 12 from patent US 5872214.
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                                                                                                                                                                                                                                                                                                                 Query Match 60.8%;
Best Local Similarity 61.9%;
Matches 13; Conservative 6
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synthetic construct
synthetic construct
synthetic construct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO 03068964-A/7.
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Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hayakawa
CC FAG1
FH Kev
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BD353840/c
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AR036420/c
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAT 04-NOV-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pierron, V.N., Allen, J.M., Allen, K.E., Phillips, T., Phelps, C.B., Fagan, R.J. and Potter, S.J. NUCLERR HORMONE RECEPTOR LIGAND BINDING DOMAIN PACENT: JP 200550010-A 4 06-JAN-2005; INPHARMATICA LIMITED OS Artificial Sequence OS Artificial Sequence PP JP 200550010-A/4 06-JAN-2005
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                                                                                                                                1. .25
/organism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."
                                                                                                                                                                                                                                                               65.8%; Score 15.8; DB 2; Length 25; larity 73.7%; Pred. No. 6.7e+04; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DD122759 24 bp DNA linear
NUCLEAR HORMONE RECEPTOR LIGAND BINDING DOMAIN.
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 24)
                                 Gunderson, K.
Probes and decoder oligonucleotides
Patent: WO 0216649-A 4341 28-FEB-2002;
Illumina, Inc. (US)
Location/Qualifiers
other sequences; artificial sequences.
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Sequence 6 from Patent W002070557.
AX538707
AX538707.1 GI:25271321
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05-MAR-2001 GB 0105402
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LBDG3 Reverse primer
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Best Local Similarity
Matches 14; Conserva
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Matches 13; Conserva
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AX538707/c
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DD122759/c LOCUS

RESULT 3

ORGANISM

VERSION KEYWORDS SOURCE

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ORIGIN

PAT 04-NOV-2005

Gaps

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PAT 29-SEP-1999

ACCESSION VERSION KEYWORDS

Gaps

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REFERENCE AUTHORS TITLE JOURNAL FEATURES

ORIGIN

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PAT 07-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BD379515 17 bp RNA linear PAT 04-NOV-2005 Method and Reagent for the Modulation and Diagnosis of CD20 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60/185516, PR
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BD37951515
BD3795151 GI:92278608
JP 2003525037-4/739.
Synthetic construct
synthetic construct
other sequences, artificial sequences.
1 (bases 1 to 17)
Blatt, L., Mcswiggen, J., Chorlila, B.M. and Harbeli, P.
Method and Reagent for the Modulation and Diagnosis of CD20 and
NGCO Gene Expression
Patent: JP 2003525037-A 739 26-AUG-2003;
Gaps
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R-2000 US 60/187128
lawrence blatt,james mcswiggen,balatto m chorlila,peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description of Artificial Sequence: Nucleic Acid FH Location/Qualifiers.
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Smith, K.E., Weinbank, R.L., Borden, L.A. and Hartig, P.R.
DNA encoding rat taurine transporter and uses thereof
Patent: US 5658786-A 23 19-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 13; DB 2; Length 17;
Pred. No. 1.5e+06;
2; Mismatches 0; Indels
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 Indels
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Pred. No. 1.1e+06;
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/organism="synthetic construct"
                                                                                                                                                         DNA
                                                                                                                                                                                                                                                                                                                                                                                  1. .25
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                  25 bp 1
equence 23 from patent US 5658786.
62320
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 Mismatches
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/db_xref="taxon:32630"
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OS Artificial Sequence
PN JP 2003525037-A/739
PD 26-AUG-2003
PF 09-FEB-2001 JP 2001558241
PR 11-FEB-2000 US 60/181797
06-MAR-2000 US 60/181797
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                                5 AGGGGCUGGUUAAGGCGU 22
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23 AGGTGCTGGTGAAGGCAT 6
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Best Local Similarity 84.6%;
Matches 11; Conservative 2
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                                                     23 AGGTGCTGGTGAAGGCAT
                                                                                                                                                                                                         GI:2480268
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Best Local Similarity 66.7<sup>3</sup>
Matches 12; Conservative
 Conservative
                                                                                                                                                                                                                                                                              Unclassified.
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harbeli
CC Dee
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 12;
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BD379515/c
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Unclassified.
I (bases 1 to 25)
Smith, K.E., Borden, L.A., Weinshank, R.L. and Hartig, P.R.
DNA encoding taurine and GABA transporters and uses thereof
Patent: US 6225115-A 23 01-MAY-2001;
Location/Qualifiers
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                                                                                                                                                                                                                       57.5%; Score 13.8; DB 2; Length 22; 70.6%; Pred. No. 6e+05; ive 3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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Selatinger, B.R., Kley,N.A. and Bianchi,A.B.
NF2 isoforms
Patent: US 5579462-A 12 26-NOV-1996;
                                                 1 (bases 1 to 22)
Selatinger, B.R., Kley, N.A. and Bianchi, A.B.
NF2 isoforms
Patent: US 5872214-A 12 16-FEB-1999;
                                                                                                                                       1. .22
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                                                                                                                                                                                                                                                                                                                                                                                                             22 bp
Sequence 12 from patent US 5578462.
129861.1 GI:1820652

    .25
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AR148541.1 GI:15112631
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                                                                                                                                                                                                                                                            12; Conservative
                                     Unclassified.
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Best Local Similarity
Matches 12; Conserv
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KEYWORDS SOURCE ORGANISM

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BD379518 17 bp RNA linear PAT 04-NOV-2005 Method and Reagent for the Modulation and Diagnosis of CD20 and
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I (bases 1 to 17)
S Blatt,L., Mcswiggen,J., Chorlila,B.M. and Harbeli,P.
NOGO Gene Expression
L Patent: UP 2003525037-A 742 26-AUG-2003;
Ribozyme Pharmaceuticals Inc
OS Artificial Sequence
PN JP 2003525037-A/742
PN JP 2003525037-A/742
PN JP 2003525037-A/742
PN G-MC-2000
PN G-MC-2000
PN G-MR-2000 US GO/181797,28-FEB-2000 US GO/185516, PR
OF-MR-2000 US GO/181718
PI Lawrence blatt,james mcswiggen,balatto m chorlila,peter PI
              Description of Artificial Sequence: Nucleic Acid FH Location/Qualifiers. Location/Qualifiers
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84.6%; Pred. No. 1.5e+06;
tive 2; Mismatches 0; Indels
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
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/organism="synthetic construct"
/mol type="unassigned RNA"
/db_xref="taxon:32630"
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Sequence 739 from Patent WO0159103.
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JP 2003525037-A/742.
synthetic construct
synthetic construct
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Best Local Similarity 84.6%;
Matches 11; Conservative
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AX215297/c
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1 (bases 1 to 17)

Blatt.L., Mcswiggen,J., Chorlila,B.M. and Harbeli,P.
Method and Reagent for the Modulation and Diagnosis of CD20 and NOGO Gene Expression
                                                                                                                                                                                                                                                                              synthetic construct
synthetic construct
other sequences; artificial sequences.

1 (bases 1 to 17)
1 Shate, .., Mcswiggen, J., Chorlila, B.M. and Harbeli, P.
Method and Reagent for the Modulation and Diagnosis of CD20 and NOGO Gene Expression
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lawrence blatt,james mcswiggen,balatto m chorlila,peter
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SArtificial Sequence

PD 26-MUG-2003

PD 26-MUG-2000

PF 10-FEB-2000 UP 2001558241

PR 11-FEB-2000 US 60/185516,

PG-MAR-2000 US 60/187128

PI hawrence blatt, james mcswiggen, balatto m chorlila, peter
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2; Mismatches 0; Indels
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PN JP 2003525037-A/741
PD 26-AUG-2003
PF 09-FEB-2001 JP 2001558241
PR 11-FEB-2000 US 60/181797, 28-FEB-2000 US
PI NAVERCA NAVEL NA
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|mol_type="unassigned RNA"
|db_xref="taxon:32630"
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Ribozyme Pharmaceuticals Inc
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JP 2003525037-A/741.
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JP 2003525037-A/740.
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Matches 11; Conservative ;
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                          1 UGAGAGGGGCUGG 13
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15 TGAGAGGGGCTGG 3
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16 TGAGAGGGCTGG 4
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PAT 07-SEP-2001

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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0159103-A 740 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
Blatt, L., Mcswiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0159103-A 739 16-AUG-2001;
RIBOZYME PHARMACEUTALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira; Bharat M. (US)
Location/Qualifiers
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/note="Nucleic Acid"
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other sequences; artificial sequences.
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Sequence 740 from Patent WO0159103.
AX215298
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1 UGAGAGGGCUGG 13

Search completed: June 19, 2007, 13:51:02 Job time: 1109 secs

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Gaps

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Query Match
Best Local Similarity 84.6%; Pred. No. 1.5e+06;
Matches 11; Conservative 2; Mismatches 0; Indels

ORIGIN

18 13.6 56.7 21 14 ACL41634 19 13.6 56.7 21 14 ACL41632 20 13.6 56.7 21 14 ACL43064 21 13.6 56.7 23 15 AEJ80377 22 13.2 55.0 19 14 ARA25301 23 13.5 55.0 19 14 ARA25301	24 13.2 55.0 20 11 ABD32143 Abd32144 26 13.2 55.0 20 11 ABD32144 Add560998 Add66487 27 13.2 55.0 20 12 ADD66487 Add66487 Add66487		34 13.2 55.0 25 10 AAD66634 35 13.2 55.0 25 12 AD061007 36 13.2 55.0 25 14 ABC90171 37 13 55.0 25 14 ABC90171	37 13 54.2 17 4 ABK00741 Abk00741 Abk00741 Abk00741 Abk00742 Abk00749 Human N 40 13 54.2 17 4 ABK00740	C 41 13 54.2 C 42 13 54.2 C 43 13 54.2 C 44 13 54.2 C 45 13 54.2	RESULT 1 ABQ11002 ID ABQ11002; XX AC ABQ11002; XX DT 11-JUN-2002 (first entry) XX Oligonucleotide adapter/capture probe 10993. XX Oligonucleotide array; adapter sequence; probe; ss. XX XX Oligonucleotide array; adapter sequence; probe; ss. XX	25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the seque given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
	nucieic - nucieic Bearch, ubing BW 1 on: June 19, 2007, 12:28:5	Title: US-10-604-726A-6034 Perfect score: 24 Sequence: 1 ugagaggggcugguuaaggcgucc 24 Scoring table: IDENTITY NUC	ij	Total number of hits satisfying chosen parameters: 4355164 Minimum DB seq length: 0	seq lengtn: ssing: Minimu Maximu Listir	N_Geneseq_200701:* Genesequ19808:* Genesequ10908:* Genesequ100018:* Genesequ100018:* Genesequ200018:* Genesequ200028:* Genesequ200028:* Genesequ200028:* Genesequ200028:* Genesequ200038:* Genesequ200038:* Genesequ200038:* Genesequ200038:* Genesequ200038:* Genesequ200048:** Genesequ20048:** Genesequ20048:** Genesequ20048:** Genesequ20068:* Genesequ20068:* Genesequ20068:* Genesequ20078:** Genesequ20078	4 13.8 57.5 17 8 ACD57816 Acd57816 HCV DI 5 13.8 57.5 17 12 AD183268 Ad183268 HCV I 6 13.8 57.5 22 2 AAT47817 Aat47817 PCR pr 7 13.8 57.5 22 2 AAX04299 Aax04299 Mouse

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25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. [1] is useful for immobilising a target nucleic acid eaquence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified arget nucleic acid with (1). The steps of above method is useful for detecting a target nucleic acid, which further
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target nucleic acid sequence, has different addresses comprising
different specific capture probes.
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29-AUG-2000; 2000US-0228854P.
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                           ABQ04715 standard; DNA;
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   ABQ04715/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising
ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further
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                                                                                                                                                                                                                                   Ouery Match 65.8%; Score 15.8; DB 6; Length 24; Best Local Similarity 73.7%; Pred. No. 1.4e+03; Matches 14; Conservative 3; Mismatches 2; Indels
                                                                    above method ar{i}_{	extsf{B}} a useful for detecting a target nucleic ac comprises detecting the presence of the modified target
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                                                                                                                                                                        Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligonucleotide adapter/capture probe 4665.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     target nucleic acid sequence, has different specific capture probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 147; 261pp; English
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29-AUG-2000; 2000US-0228854P.
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Best Local Similarity 73.7%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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comprises detecting the presence of the modified target nucleic acid
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                                             Length 24;
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                       Sequence 24 BP; 5 A; 10 C; 2 G; 7 T; 0 U; 0 Other;
                                             Score 15.8; DB 6;
Pred. No. 1.4e+03;
                                                                     3; Mismatches
                                                                                                                                                                                                                                    Oligonucleotide adapter/capture probe 349.
                                                                                          20
                                               65.8%;
                                                                                          2 GAGAGGGCUGGUUAAGGC
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25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ0010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic and and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid.
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invention relates to an oligonucleotide array (I)
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                                                                                                                                                                                                                 Sequence 24 BP; 5 A; 10 C; 2 G; 7 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                           Score 15.8; DB 6;
Pred. No. 1.4e+03;
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Pred. No. 1.4e+03;
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                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   target nucleic acid sequence, nas different specific capture probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 244; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                  2 GAGAGGGCUGGUUAAGGC 20
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29-AUG-2000; 2000US-0228854P.
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                                                                                                                                                                                                                                                                                                        14; Conservative
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nes 14; Conservative
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                                                                                                                                                                                                                                       detecting a
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                                        2000US-0227948P.
2000US-0228854P.
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29-AUG-2000; 2000US-0228854P.
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27-AUG-2001; 2001WO-US026519
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                                          25-AUG-2000;
29-AUG-2000;
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RESULT 5 ABQ11043/c

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Potter SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising different specific capture probes.
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                                                                                                                                                                         Oligonucleotide adapter/capture probe 12570
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GAGAGGGTTGGTTAAGGC 23
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29-AUG-2000; 2000US-0228854P.
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ABQ12579 standard; DNA; 25
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sunderson K;
                                                                                                                                            11-JUN-2002
                                                                                                                                                                                                                                                                                         28-FEB-2002
                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAL50117;
                                                                                                                  ABQ12579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAL50117/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                        ABQ12579,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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8 a a

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorders
                     immunosuppressive; virucide; fungicide; antibacterial; antiparastit; cardiant; antidepressant; antidiabetic; vasotropic; antiliflammatory; nephrotropic; cytostatic; antilipemic; hypotensive; antiallergic; antithyroid; anorectic; osteopathic; analgesic; antiposcriatic; vulnera cerebroprotective; hamostatic; thrombolytic; cardiovascular disorder; neurological disorder; infection; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mellitus, osteoporosis, lipid metabolism disorders, hyperthyroidism, hyperparathyroidism, hypercalcaemia, hypercholesterclaemia, hypercholesterclaemia, hypercholesterclaemia, hyperthyroidism, hyperthyroidism, hyperthyroidism, hyperthyroidism, hyperthyroidism, hyperthyroidism, hyperthyroidism, nostey, renovascular hypertension, dermatological disorder including acne, eczema and wound healing, negative effects of aging, acquired immunodeficiency syndrome (AIDS), viral, bacterial, fungal an parasitic infections, and other pathological conditions, particularly those in which nuclear hormone receptors are implicated. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Allen JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence is a PCR primer used to isolate the coding sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New CAB55953.1 or LBDG3 polypeptide, useful as a nuclear hormone ligand-binding domain, or for manufacturing of a medicament for diagnosing or treating cell proliferative disorders or autoimmune/inflammatory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             brain injury, stroke, amyotrophic lateral sclerosis, anxiety, dep
and pain, developmental disorders, metabolic disorders including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phelps CB, Phillips T, Pierron VN, Allen KE,
antiarrhythmic; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 24 BP; 7 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 64; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 AGAGGGCUGGUUAAGGCGUC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAGGGCTTATTAACTCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAR-2002; 2002WO-GB000937.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-MAR-2001; 2001GB-00005402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 Similarity 61.9%;
13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INPH-) INPHARMATICA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADA24254 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-698731/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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Modulating, in a host cell, a protein-protein interaction between first protein, PRAK, (MAPKAPKS) and second protein, ERK3, (extracellular signal-regulated kinase 3) by administering modulating compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 39; 296pp; English
                             20-OCT-2003; 2003US-00690276
                                                                                                                                                                                                                                                                                                                     (MYRI-) MYRIAD GENETICS
                                                                                                                                                                                                                                                                                                                                                                           WPI; 2005-371623/38.
                                                                                                                                                                                                                                                                                         18-MAR-2002;
                                                                                                                                                                                                                                                                                                                                              Cimbora D,
                                                                                                                                                                                                                     DEC-200
                                                                                                                                                                                                                                                                            4-MAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                  absence of a specific substance in a food by performing PCR with primers which are designed on the basis of data obtained from a part of a gene of the specific substance. Also described: (1) a similar method for detecting a trace component contained in a food, or for identifying a harmful allergen specific to a consumer of such substance by performing a PCR with primers which are designed on the basis of data obtained from a part of a gene of the specific substance; (2) primers for PCR applicable in food testing which are designed on the basis of data obtained from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   part of a gene of the specific substance, and (3) kits for determining concentration of a specific substance in the food containing the primers. The methods are useful for testing foods, which can be used in detecting trace components or identifying specific harmful allergens in (processed) foods, particularly applicable in food safety and management. The present sequence represents a PCR primer for a Fagopyrum esculentum major allergenic storage protein designated FAGGMCI, which is used in the
Major allergenic storage protein FAGAG1 PCR primer FAG19 SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       present invention describes a method for testing the presence or
                                                                                                                                                                                                                                                                                                                PCR-based method for testing foods using specific primers designed genes of target substance, useful in detecting trace components or identifying specific harmful allergens in (processed) foods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 21;
                             food testing; allergen; PCR primer; Fagopyrum esculentum;
major allergenic storage protein; FAGAG1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 14.4; DB 9;
Pred. No. 6.2e+03;
4; Mismatches 1;
                                                                                                                                                                                                                                                             Hayakawa K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exemplification of the present invention
                                                                                                                                                                                                                                                             Miyatake K,
                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 10; 38pp; Japanese
                                                                                                                                                                                                                               (NISS ) NISSHIN SEIFUN GROUP INC.
                                                                                                                                                                         26-SEP-2002; 2002WO-JP009982
                                                                                                                                                                                                     15-FEB-2002; 2002JP-00038930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60.0%;
68.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGCTGGTTATGGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGCUGGUUAAGGCGU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 68.8
nes 11; Conservative
                                                                                                                                                                                                                                                           Yamakawa H, Suzuki E,
                                                                                     Fagopyrum esculentum.
                                                                                                                                                                                                                                                                                       WPI; 2003-637145/60.
                                                                                                                  WO2003068964-A1
                                                                                                                                             21-AUG-2003
                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
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Bush A;

Bartel P, Mauck K,

Heichman K,

2001US-0259571P. 2001US-0259572P. 2001US-0276179P. 2001US-0277013P. 2001US-0307233P.

2001US-00024599

2002US-00100503

99US-0168379P 2000US-0185056P 2000US-00727384 2000US-0255063P 2000US-0256986P

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The invention relates to a method for modulating, in a host cell, a protein-protein interaction between a first protein which is PRAK (P38-regulated/activated protein kinase or MAPKAPK5) and a second protein which is ERK3 (extracellular signal-regulated kinase 3). The method comprises administering to the cell a compound capable of modulating the protein-protein interaction. The method is useful in modulating in a host cell a protein-protein interaction between a first protein which is PRAK and a second protein which is ERK3 for treating inflammation or inflammatory disorders, e.g., asthma, rheumatoid arthritis, juvenile chronic arthritis, inflammatory bowel disease, gastritis, colitis, ulcerative colitis, inflammatory bowel disease, proctitis, pelvic inflammatory disease, systemic lupus erythematosus, rhinitis, conjunctivitis, scleritis, chronic inflammatory polymeuropathy, Tertiary Lyme disease, psoriasis, dermantisor eccema. In the exemplification of the present invention examples of antisense oligonucleotides specific to nucleic acids encoding individual proteins in tables 1 to 82 are provided
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human DNA probe used to immobilise CpG methylated DNA SeqID 474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.2%; Score 14.2; DB 14; Length 20; 68.4%; Pred. No. 7.7e+03; Live 3; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 4 A; 10 C; 2 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acide encoding individual protein
in SEQ ID NOS:11-223 (ADZ97857-ADZ98069).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 AGGGGCUGGUUAAGGCGUC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ~
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGGCTGGTAATGGAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 68.4 tes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADJ13347;
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ADJ13347/c
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protein interaction; antisense oligonucleotide; ss.

US2005112118-A1 Homo sapiens

Human antisense oligonucleotide SEQ ID NO:39

28-JUL-2005 (first entry)

ADZ97885 standard; DNA; 20

ADZ97885/c

ADZ97885;

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The invention relates to novel murine and human testis specific serine proteases (Tespec PRO; AAB03156-B03160) and to cDNAs encoding them corrected and to cDNAs encoding them (AAA61558-A61562). It also encodings see expression vectors and host cells comprising a nucleotide sequence encoding a protease of the invention, inhibitors of the proteases and antibodies against the proteases. The novel proteases are members of the trypsin family of serine proteases, having the serine and histidine active site signatures characteristic of this family. The proteases are specifically expressed in mature testis and participate in the differentiation and maturation of sperm. The proteases are potentially useful for the development of pharmaceuticals for the treatment of male infertility and other male reproductive disorders, and for the development of contraceptives. They may also be used as reagents for the displaneis of male infertility. Sequences AAA61593 represent RACE (rapid amplification of cDNA ends) PCR primers used in the isolation of cDNA ends) PCR
                                                                                                                                                                                                                                                         psin family serine proteases expressed specifically in mature testis development of methods for diagnosis and treatment of sterility and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 14.2; DB 3; Length 25; Pred. No. 7.9e+03; 1ndels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human microarray DNA oligonucleotide SEQ ID NO 82768.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25 BP; 4 A; 2 C; 10 G; 9 T; 0 U; 0 Other;
                                                                                                                            (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                      Example 9; Page 45; 121pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGGGCUGGUUAAGGCGU 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GATGGGCTAGTTAAGTCGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACI82777 standard; DNA; 25 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAR-2001; 2001US-0276759P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-MAR-2002; 2002US-00098263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.2%;
63.2%;
                                             99WO-JP006111
                                                                                      98JP-00313366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cross-species comparison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                Prypsin family serine
                                                                                                                                                                                                                     WPI; 2000-365604/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                           for contraception.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2003104410-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                   04-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-OCT-2003
                                           02-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mittmann MP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUN-2003
11-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AAA61561
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                                                                                                                                                                              Senoo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified macromolecules. Specifically, it refers to a high throughput method for the parallel analysis of many potential sites of chemical modification (e.g. methylation) in DNA. The present invention describes treating the DNA with one or more chemical reagents that result in different base sequences depending upon the presence or absence of the probles is provided to hybridise with and select the altered DNA sequences that comprise the modifications of interest such as a CpG island. In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    particular, this invention refers to analysing the methylation pattern of a region of the promoter for the tumour suppressor gene p16 from two human lung tumour cell lines H69 and H1618. This oligonucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Analysis of chemical modification of DNA involves obtaining sample of DNA to be analyzed, treating DNA with chemical reagents that result in different base sequences, and determining sequence of resulting DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Tespec PRO-3; testis specific serine protease; trypsin family serine protease; mature testis; sperm differentiation; sperm maturation; male infertility; sterility; reproductive disorder; contraception; rapid amplification of cDNA ends; RACE PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a human DNA probe used to immobilise CpG methylated DNA of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to a novel method for analysing chemically
    probe; ss; chemical modification; methylation; array; CpG island;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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Pred. No. 7.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21 BP; 6 A; 11 C; 1 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Tespec PRO-3 5' RACE PCR primer, hPRO3-D.
                                                                                                                                                                                                                                                                                                                                                                                                   Balog RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                           tumour suppressor; pl6; human; H69; H1618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; SEQ ID NO 474; 210pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   Luebke KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 UGAGAGGGCUGGUUAAGG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
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                                                                                                                                                                                                                                           27-JUN-2001; 2001US-0301370P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                   Sarner HR, Minna JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-874843/81.
                                                                                                                                                                                                                                                                                         GARNER H R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                             MINNA J D.
LUEBKE K J.
                                                                                                                                                                                                                                                                                                                                                          (BALO/) BALOG R P.
                                                                                                               JS2003152950-A1
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                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                             (MINN/)
(LUEB/)
                                                                                                                                                                                                                                                                                         GARN/)
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AAA61591

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Gaps

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Lee P;

Pavco P,

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The present invention relates to nucleic acid molecules which modulate
the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
are nucleic acid decoy molecules and aptamers that bind to HBV reverse
transcriptase and/or HBV reverse transcriptase primer sequences, as well
as oligonucleotides that specifically bind the Enhancer I region of HBV
DNA. The nucleic acids may be used to modulate the expression of HBV
compounds and/or potential therapies directed against HBV, and compounds
that modulate the expression and/or replication of HCV. The compounds
that modulate the expression and/or replication of HCV. The compounds
chat modulate the expression and for replication of HCV. The compounds
chat modulate the expression and for replication of HCV and compounds
chat modulate the expression and for replication of HCV. The compounds
chat modulate the activities and HCV infection, replication and gene
expression such as cirrhosis, liver failure, and hepatocellular
carcinoma. The present sequence represents a substrate for one of the HCV
bundary and present sequence represents a substrate for one of the HCV
bundary and present minus strand DNAzyme sequences disclosed in the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV; HCV infection; type I interferon; DNAzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.5%; Score 13.8; DB 8; Length 17; 70.6%; Pred. No. 1.2e+04; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17 BP; 4 A; 9 C; 1 G; 0 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                     Mcswiggen J, Morrissey D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCV DNAzyme substrate sequence #514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 243; 387pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADI83268 standard; RNA; 17 BP
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08-JUN-2001; 2001US-0296876P.
24-OCT-2001; 2001US-0335059P.
05-DEC-2001; 2001US-0337055P.
                                                                                                                RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGCAGGTTAAGGTGT
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(first entry)
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Matches 12; Conservative
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Β;
                                                                                                                                                                MACEJAK D.
MCSWIGGEN J.
MORRISSEY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-229207/22.
                                                                                                                                                                                                                                                                                                                                                                                                               Roberts
                                                                                                                                                                                                                                                                           LEE P.
DRAPER K.
ROBERTS E.
                                                                                                                                                                                                                                                                                                                                                                                        Macejak
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                                                                                                                                                                                                                                                    PAVCO P.
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                                                                                                                                            BLATT
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03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection.
                                                                                                                                                                                                                                                                                                                                                                                                               Draper K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention
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                                                                                                                                                                                                                                                                                                                                                                                     Blatt L,
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                                                                                                                                                                                                                     (MORR/)
(PAVC/)
(LEEP/)
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(ROBE/)
                                                                                                                                      (BLAT/)
(MACE/)
(MCSW/)
                                                                                                                (RIBO-)
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                                                                                                                                                                                                                                      The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more hybridising at least one or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes and expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dotblot hybridisation to identify or detect the sequence or specific acid probes is useful in in situ hybridisation, in Southern, Northern or dotblot mitations of any gene, in mapping the S' terminin of mRNA molecules by primer extensions or in screening companies or subclones for additional subclones containing segments of DNA that have been incorporated in the microarray. Note make and proportions of any pages, the sequence presented is one of the nucleic acid probes and proportions in the microarray.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at segdata.uspto.goc/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV; RNA stability; RNA expression; RNA synthesis; antiennse; enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; inzyme; amberzyme; G-cleaver ribozyme; decoy molecule; aptamer; HBV reverse transcriptase; Enhancer I region; viral replication; degenerative; disease state; HBV infection; HCV infection; clirhosis; liver failure; hepatocellular carcinoma; hepatotropic; cytostatic; virucide; antiinflammatory; substrate; ss.
                                                                              New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                         Claim 1; SEQ ID NO 82768; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNAzyme substrate sequence #514.
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08-JUN-2001; 2001US-00877478
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                            WPI; 2003-567953/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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ACD57816/c
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03-JUL-2003.

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Enzymatic nucleic acid molecules which specifically cleave RNA derived from hepatitis C virus (HCV), useful for the treatment of HCV infections, especially in combination with type I interferon therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an enzymatic nucleic acid molecule which specifically cleaves RNA derived from hepatitis C virus (HCV), in which the binding arms of the enzymatic nucleic acid molecule comprises sequences complementary to any of the defined substrate sequences given in the specification. The nucleic acid molecule may be administered for the treatment of HCV infections, especially in combination with type I interferons. The present sequence represents a HCV DNAzyme substrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Revised record issued on 22-SEP-2005 : No correction was made to this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 57.5%; Score 13.8; DB 12; Length 17; Best Local Similarity 70.6%; Pred. No. 1.2e+04; Matches 12; Conservative 3; Mismatches 2; Indels C
                                                                                                                                                                                                                             Roberts E, Pavco PA, Macejack D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 BP; 4 A; 9 C; 1 G; 0 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 514; 198pp; English
                                   18-DEC-2000; 2000US-00740332.
                                                                         18-DEC-2000; 2000US-00740332
                                                                                                                                                                                                                               Blatt L, Mcswiggen J,
                                                                                                          (BLAT/) BLATT L.
(MCSW/) MCSWIGGEN J.
(ROBE/) ROBERTS E.
(PAUC/) PAUCO P.A.
(MACE/) MACEJACK D.
                                                                                                                                                                                                                                                                   WPI; 2004-031273/03
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Gaps

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Search completed: June 19, 2007, 13:01:30 Job time : 249.5 secs

6 GGGGCUGGUUAAGGCGU 22

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Sequence 12, Application US/08179738
Patent No. 5578462
GENERAL INFORMATION
APPLICANT: Selzinger, Bernd R.
APPLICANT: Rley, Nikolai A.
APPLICANT: Bianchi, Albert B.
TITLE OF INVENTION: No. 5578462el NF2 Isoforms
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 UGAGAGGGCUGGUUAAGGCGU 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 TGAGATGAGCTGCTTAACGAGT 1
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STREET: 635 Bryant Street
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 54.5
Matches 12; Conservative
  TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                         US-09-396-196G-15707/c
  US-09-396-196G-15707
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US-08-179-738-12/c
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Query Match
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29254, A
11, Appl
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9132, Ap
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Appl
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                                                                              June 19, 2007, 12:53:27 ; Search time 256 Seconds (without alignments) 175.760 Million cell updates/sec
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| KBNC Celerra SIDS3/ptodata/2/ina/1 COMB.seq:*
| KBNC Celerra SIDS3/ptodata/2/ina/5 COMB.seq:*
| KBNC Celerra SIDS3/ptodata/2/ina/6 COMB.seq:*
| KBNC Celerra SIDS3/ptodata/2/ina/6 COMB.seq:*
| KBNC Celerra SIDS3/ptodata/2/ina/6 COMB.seq:*
| KBNC Celerra SIDS3/ptodata/2/ina/R COMB.seq:*
| KBNC Celerra SIDS3/ptodata/2/ina/PCTUS COMB.seq:*
| KBNC Celerra SIDS3/ptodata/2/ina/PCTUS COMB.seq:*
| KBNC Celerra SIDS3/ptodata/2/ina/R COMB.seq:*
| KBNC Celerra SIDS3/ptodata/2/ina/R COMB.seq:*
| KBNC Celerra SIDS3/ptodata/2/ina/R COMB.seq:*
| KBNC Celerra SIDS3/ptodata/2/ina/Backfiles1.seq:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
             GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-396-196G-58488
US-09-396-196G-73489
US-09-396-196G-78586
US-09-396-196G-122139
US-09-422-978-9132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-396-196G-15707
US-08-179-738-12
US-08-25-8145-12
US-08-29-343-361-23
US-09-343-361-23
US-09-346-1259B-31
US-10-059-579A-123
US-09-166-119
US-09-166-119
US-09-313-312-119
US-09-313-313-313
US-09-313-313-313
US-09-313-313-313
US-09-313-057-51
US-09-313-057-51
US-09-396-196G-3644
US-09-396-196G-3644
US-09-396-196G-3644
US-09-396-196G-3644
US-09-396-196G-3644
                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                   1403666 segs, 935554401 residues
                                                                                                                                                         24
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                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                            nucleic search, using sw model
                                                                                                                                                          1 ugagagggcugguuaaggcgucc
                                                                                                                                                                              IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                    US-10-604-726A-6034
24
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                                                                                                                                                                                                                                                                 seq length: 0
seq length: 25
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Match
                                                                                                                                                                                 Scoring table:
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                                                            OM nucleic -
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Maximum DB
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3, Appli
66, Appl
1593, Ap
7, Appli
7, Appli
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Sequence 14034, A
Sequence 42202, A
                                                                                                                                                                                                             Sequence 8376, Ap
Sequence 4032, Ap
Sequence 4032, Ap
                                                                                                                                                                                                                                                                                                     Sequence 35, Appl
Sequence 2, Appli
                                                                                                                                                                                               Sequence 44091,
                                                                                                                                                                                                                                                           Sequence 4032,
Sequence 152,
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                                                                                            Sequence 3
Sequence 6
Sequence 1
Sequence 7
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.3%; Score 14; DB 3; Length 25; 54.5%; Pred. No. 2e+03;
| Sequence 1570/7, Application US/09396196G |
| Sequence 15707, Application US/09396196G |
| Sequence 15707, Application US/09396196G |
| Patent No. 6821724 |
| GENERAL INFORMATION: |
| APPLICANT: David Mack |
| APPLICANT: David Lockhart |
| APPLICANT: DAVIG LOCKHART |
| FILE REFERENCE: 3101.1 |
| CURRENT APPLICATION NUMBER: 05/100,678 |
| PRIOR PILING DATE: 1998-09-17 |
| NUMBER OF SEQ ID NOS: 127806 |
| SEQ ID NO 15707 |
| LENGTH: 25 |
| LENGTH: 25
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Length 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Smith, Kelli E.
APPLICANT: Borden, Laurence A.
APPLICANT: Harrig, Paul R.
APPLICANT: Weinshank, Richard L.
TITLE OF INVENTION: DNA ENCODING TAURINE AND GABA
TITLE OF INVENTION: TRANSPORTERS AND USES THEREOF
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 13.2; DB 2;
Pred. No. 4.9e+03;
3; Mismatches 3;
                                                                                                                                                                                                                              .5e+03
                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                     Query Match 57.5%; Score 13.8; Best Local Similarity 70.6%; Pred. No. 2.5 Matches 12; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,814E
FILING DATE: DECEMBER 19, 1994
CLASSIFCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40558-B-PCT-TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSEE: Cooper & Dunham Lip
1: 1185 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23, Application US/08295814E
Patent No. 5658786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                               3 AGAGGGCUGGUUAAGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.0%;
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Best Local Similarity 66.7
Matches 12; Conservative
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                               single
                                                                     TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                               TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-295-814E-23/C
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US-09-343-361-23/c
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                                                                                                                                                             US-08-628-145-12
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                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
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                                                                                                                                                         CURRING SISIEM: PURSONING SISIEM: SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

APPLICATION UNDER: US/08/179,738 FILING DATE: U0-JAN-1994
CLASSIFICATION: 530
ATTONREY/AGENT INFORMATION:
NAME: RODINS, RODERTA INFORMATION:
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5998-0017
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 17-8999
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHRRACTERISTICS:
LENGTH: 22 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NS.011.

(S.03-628-145-12/c
; Sequence 12, Application US/08628145
; Patent No. 5872214
; GENERAL INFORMATION:
; APPLICANT: Seizinger, Bernd R.
APPLICANT: Rley, Nikolai A.
; APPLICANT: Bianchi, Albert B.
; TITLE OF INVENTION: No. 5872214el NF2 Isoforms
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robins
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,145
FILING DATE: 04-APR-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/179,738
FILING DATE: 10-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 33,206
REFERENCE/DOCKET NUMBER: 53
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 AGAGGGCUGGUUAAGG 19
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17 AGAGGAGCTGGTTCAGG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Reed & Robins
STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
COUNTRY: U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (415) 327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: .cDNA
US-08-179-738-12
           California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                   94301
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TYPE: DNA
ORGANISM: Artificial sequence
  US-08-460-751-27
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LENGTH: 19
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                                    GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Smith, Kelli E. et al

APPLICANT: Smith, Kelli E. et al

TITLE OF INVENTION: DNA Encoding Taurine and GABA Transporters and Uses

TITLE OF INVENTION: Thereof

FILE REFERENCE: 40558-D

CURRENT APPLICATION NUBER: US/09/343,361

CURRENT FILING DATE: 1999-06-30

NUMBER OF SEQ ID NOS: 28

SOFTWARENT FILING DATE: 1999-06-30

LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Schneider, Michael
APPLICANT: Schneider, Michael
APPLICANT: Glucksmann, Sandra
TITLE OF INVENTION: IDENTIFICATION OF POLYCYSTIC KIDNEY
TITLE OF INVENTION: DISEASE GENE, DIAGNOSTICS AND TREATMENT
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: primer
                                                                                                                                                                                                                                                                                                                                                                                                                               55.0%; Score 13.2; DB 3; Length 25; 66.7%; Pred. No. 4.9e+03; ative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,751
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/413,580
FILING DATE: 03-MRR.1995
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7638-005
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27, Application US/08460751
Patent No. 5891628
GENERAL INFORMATION:
APPLICANT: Reeders, Stephen
Sequence 23, Application US/09343361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 AGGGGUGGUUAAGGCGU 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 AGGTGCTGGTGAAGGCAT 6
                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 66141 PENNIE
ORMATION FOR SEQ ID NO:
EQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 base pairs
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: New York
TRY: U.S.A.
10036-2711
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 relephone:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                          FEATURE:
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GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: EVRON, B1a
APPLICANT: DOOLEY, William C.
APPLICANT: DAVIDSON, Nancy
APPLICANT: PACKLER, Mary Jo.
TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY
FILE REPERENCE: JUN1630-1.28
CURRENT APPLICATION NUMBER: US/10/059,579A
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                                                    Gaps
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  Length 19;
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                                                    Indels
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  Score 12.8; DB 2;
Pred. No. 7.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 12.8; DB 3;
Pred. No. 7.6e+03;
3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Borini, James A
APPLICANT: Borowsky, Beth B
APPLICANT: Adham, Nika
APPLICANT: Adham, Nika
APPLICANT: Thompson, Thelma O.
TITLE OF INVENTION: DNA Encoding SNORF25 Receptor
FILE REFERENCE: 1795/56095-B/JPW/ADM
CURRENT APPLICATION NUMBER: US/09/641,259B
CURRENT FILING DATE: 2002-03-12
                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/USOO/04413
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 09/387,699
PRIOR FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: US 09/255,376
PRIOR FILING DATE: 1999-02-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 09/771,357
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 136
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-059-579A-123/c
; Sequence 123, Application US/10059579A
; Patent No. 6835541
                                                                                                                                                                                                                                             US-09-641-259B-31/c; Sequence 31, Application US/09641259B; Patent No. 6468756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Primer/ Probe US-09-641-259B-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.3%;
68.8%;
Query Match
Best Local Similarity 62.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.1
SEQ ID NO 31
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 GAGGGCTGCTTAATG
                                                                                                    GCUGGUUAAGGCGUCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 53.3'
Best Local Similarity 68.8'
Matches 11; Conservative
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SEQ ID NO 51
LENGTH: 20
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APPLICANT: Baker, Brenda
APPLICANT: Bennett, C. Frank
APPLICANT: Bunnett, C. Frank
APPLICANT: Butler, Madeline M.
APPLICANT: Butler, Madeline M.
APPLICANT: Shanahan, William R.
TITLE OF INVENTION: ANTISENSE OLICONUCLEOTIDE MODULATION OF TNF-a EXPRESSION
FILE REFERENCE: ISPH-03.2
CURRENT APPLICATION NUMBER: US/09/166,186A
CURRENT FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 250
SEQ ID NO 119
LENGTH: 20
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TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-
TITLE OF INVENTION: EXPRESSION
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                                                                                      Score 12.6; DB 3; Length 19;
Pred. No. 9.1e+03;
4; Mismatches 4; Indels
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CURRENT APPLICATION NUMBER: US/09/313,932A
CURRENT FILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 501
SEQ ID NO 119
LENGTH: 20
                      ; OTHER INFORMATION: PCR antisense primer US-10-059-579A-123
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COTHER INFORMATION: antisense sequence
US-09-166-186-119
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                                                                                                                                                                                                                                                                                                                                                         Sequence 119, Application US/09166186A Patent No. 6080580
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                                                                                                                                                                                                                                         19 GAAGGGGTAGTTAAGGGGT
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APPLICANT: Bennett, C. Frank
APPLICANT: Butler, Madeline M.
                                                                                           Query Match
Best Local Similarity 57.9%;
Matches 11; Conservative
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FEATURE:
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4 GAGGGCUGGUUAAGGCGU 22

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GENERAL INFORMATION:
APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.
APPLICANT: KIM, Cheol Min
APPLICANT: PARK, Hee Kyung
TITLE OF INVENTION: Oligonucleotide for detection and identification of Mycobacteria
FILE REFERENCE: PP05020/PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: sequence of probe or primer for detecting Mycobacterium abscessus
US-09-980-052-51
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APPLICANT: Chader, Gerald J
APPLICANT: Chader, Sofia P
APPLICANT: Becerra, Sofia P
APPLICANT: Johnson, Lincoln V
APPLICANT: Johnson, Lincoln R
APPLICANT: Johnson, Lincoln R
APPLICANT: Johnson, Lincoln R
APPLICANT: Codinguez, Ignacio R
TITLE OF INVENTION: RETINAL PIGMENTED EPITHELIUM DERIVED NEUROTROPIC FACTOR
FILE REPERENCE: 2026-4230431
CURRENT APPLICATION NUMBER: US/08/520,373D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 20;
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Pred. No. 9.1e+03;
3; Mismatches 4;
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PRIOR APPLICATION NUMBER: KR 10-1999-0019631
PRIOR PILING DATE: 1999-05-29
PRIOR APPLICATION NUMBER: KR 10-1999-0019632
PRIOR PILING DATE: 1999-05-29
PRIOR PLILING DATE: 1999-05-29
PRIOR PLLING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 243
SOFTWARE: KOPACHIN 1.71
                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/980,052
CURRENT FILING DATE: 2001-11-28
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PRIOR FILING DATE: 1995-01-25
PRIOR APPLICATION NUMBER: 08/279,979
PRIOR FILING DATE: 1994-07-25
PRIOR APPLICATION NUMBER: 07/894,215
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PRIOR APPLICATION NUMBER: 07/952,796
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; Sequence 31, Application US/08520373D
                                                                                                             US.09-980-052-51
; Sequence 51, Application US/09980052
: Patent No. 6670130
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illarity 63.2%;
Conservative
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20 GGGGGCGGGTTGAGGGGT
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NUMBER OF SEQ ID NOS: 34
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SEQ ID NO 31
LENGTH: 21
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Best Local Similarity
Matches 12; Conserv
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US-09-396-196G-3644
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                                                                 LENGTH:
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                                                             Description of Artificial Sequence: SYNTHETIC
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                                                                                                                                                                     Score 12.6; DB 3; Length 21;
Pred. No. 9.2e+03;
3; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 45, Application US/09443067
Patent No. 6627794
GENERAL INFORMATION:
APPLICANT: COMMONEBLITH SCIENTIFIC AND INDUSTRIAL RESEARCH
APPLICANT: ORGANISATION
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EARLIER APPLICATION NUMBER: US 08/976, 222
EARLIER PILLING DATE: 1999-11-12
EARLIER FILLING DATE: 1997-11-21
EARLIER PILLING DATE: 1997-019
EARLIER PILLING DATE: 1998-05-19
EARLIER FILLING DATE: 1995-05-23
EARLIER FILLING DATE: 1995-05-23
EARLIER FILLING DATE: 1995-05-23
EARLIER FILLING DATE: 1995-05-05-05
EARLIER FILLING DATE: 1997-05-19
EARLIER FILLING DATE: 1997-05-19
EARLIER FILLING DATE: 1995-09-26
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PATENTING UNIVERSES OF SEQ ID NOS: 49
SEQ ID NO 45
LENGTH: 25
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CURRENT FILING DATE: 1999-09-15
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Partent No. 6821724
GENERAL INFORMATIO:
APPLICANT: Michael Mittmann
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PRIOR FILING DATE: 1998-09-17
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ORGANISM: Artificial Sequence
TYPE: DNA
ORGANISM: Artificial Sequence
                                                    OTHER INFORMATION: DESCRIPC: OTHER INFORMATION: PRIMER COTHER INFORMATION: PRIMER 1 US-08-520-373D-31
                                                                                                                                                                     Query Match
Best Local Similarity 63.2
Matches 12; Conservative
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David Lockhart
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Matches 12; Conserv
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US-09-443-067-45
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APPLICANT:
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Pred. No. 9.5e+03;
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Pred. No. 9.5e+03;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/396,196G
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
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US-06-1366-196G-29254
; Sequence 29254, Application US/09396196G
; Patent No. 6821724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
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                                                                                                                                                        52.5%;
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                                                                                                                                         Query Match
Best Local Similarity 68.41
Best Local 3; Conservative
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Best Local Similarity 57.9
Matches 11; Conservative
                                                                             TYPE: DNA ORGANISM: Mus musculus
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June 19, 2007, 13:01:01; Search time 1262 Seconds (without alignments) 233.679 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMC_Celerra_SIDS3/prodate3/2/pubpna/US10E_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US10E_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US10E_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US10G_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US11A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US11A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US11A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US11A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US11A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US11A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US11A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US11A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US11A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US11A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US11A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US11A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US11A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US11A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US11A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US11A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US11A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US11A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US11A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US11A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US1A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US1A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US1A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US1A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US1A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US1A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US1A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US1A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US1A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US1A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US1A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US1A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodate3/2/pubpna/US1A_PUBCOMB.seq./EMC_Celerra_SIDS3/prodat
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/BMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seg:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /EMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_PUBCOMB.seq:*/EMC_Celerra_SIDS3/ptodata/2/pubpna/USO8_PUBCOMB.seq:*/EMC_Celerra_SIDS3/ptodata/2/pubpna/USO9A_PUBCOMB.seq:*/EMC_Celerra_SIDS3/ptodata/2/pubpna/USO9B_PUBCOMB.seq:/EMC_Celerra_SIDS3/ptodata/2/pubpna/USO9C_PUBCOMB.seq:/EMC_Celerra_SIDS3/ptodata/2/pubpna/USO9C_PUBCOMB.seq:/EMC_Celerra_SIDS3/ptodata/2/pubpna/USO0B_PUBCOMB.seq:/EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq:/EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq:/EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq:/EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq:/EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq:/EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq://EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq://EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq://EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq://EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq://EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq://EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq://EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq://EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq://EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq://EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq://EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq://EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq://EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq://EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq://EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq://EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq://EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq://EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq://EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq://EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq://EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq://EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq://EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq://EMC_Celerra_SIDS3/ptodata/2/pubpna/USOOB_PUBCOMB.seq://EMC_Celerra_SIDS3/pto
GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd.
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Maximum Match 1008
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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length: 25
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Maximum DB seq
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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d	713202	888593,	365, Ap	4341, Ā	751276	508584	648052	310484	310485	310486	310487	594029	1286104	1056699	594065	1286102	62329,
Description	Sequence 713202	Sequence	Sequence 365,	Sequence 4341,	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence 62329,
. QI	US-11-036-317-713202	JS-10-719-900-888593	JS-09-940-185-365	JS-09-940-185-4341	US-11-036-317-751276	US-11-036-317-508584	US-11-036-317-648052	US-10-310-914A-310484	US-10-310-914A-310485	US-10-310-914A-310486	US-10-310-914A-310487	US-10-310-914A-594029	US-10-310-914A-1286104	US-10-310-914A-1056699	US-10-310-914A-594065	US-10-310-914A-1286102	US-10-719-900-62329
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% Query Match Length DB	25	25	24	25	25	25	25	21	21	21	21	21	21	22	24	24	25
Query Match	69.2	67.5	65.8	65.8	65.8	65.0	65.0	63.3	63.3	63.3	63.3	63.3	63.3	63.3	63.3	63.3	63.3
Score	16.6	16.2	15.8	15.8	15.8	15.6	15.6	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2
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U	24	15	62.5	25		US-11-036-317-798014	Sequence 798014,
υ	25	14.8	61.7	21		US-10-310-914A-752575	Sequence 752575,
O	26	14.8	61.7	22	11	US-10-310-914A-175870	Sequence 175870,
	27	14.6	8.09	21	Ξ	US-10-310-914A-371120	Sequence 371120,
	28	14.6	8.09	23		US-10-310-914A-707100	
υ	59	14.6	8.09	23	11	US-10-310-914A-1006052	Sequence 1006052,
υ	30	14.6	8.09	24		US-10-469-866-23	N
	31	14.6	8.09	24	1	US-10-310-914A-224322	Sequence 224322,
	32	14.6	8.09	25	œ	US-10-719-956-115625	Sequence 115625,
	33	14.6	8.09	52	œ	US-10-719-956-115627	Sequence 115627,
O	34	14.6	8.09	25		US-10-719-900-888594	Sequence 888594,
	35	14.6	60.8	25	13	US-11-036-317-892224	a)
υ	36	14.6	8.09	25		US-11-036-317-966783	Sequence 966783,
	37	14.6	8.09	52	12	US-11-121-849-363	Seguence 363, App
υ	38	14.4	0.09	21		US-10-504-589A-7	Sequence 7, Appli
	39	14.4	0.09	24		US-10-310-914A-1339473	
	40	14.4	0.09	25	œ	US-10-719-956-605791	
	41	14.4	0.09	25	8	US-10-719-956-605792	
	42	14.4	0.09	25	13	US-11-036-317-213436	Sequence 213436,
	43	14.4	0.09	25	Ë	US-11-036-317-884459	Sequence 884459,
ť	44	4	2.0	6	-	10-310-914A-10566	105
)	45	4	59.2	19	14	-11-083-784-1176587	equence 117
						ALIGNMENTS	
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ns.	11-03	US-11-036-317-713202/c	13202/c				
Š.	ednen	ce 7132(02, Appli	cation	n US	Sequence 713202, Application US/11036317	
Δ. ξ	ublic	Publication No. US2	o. US2005	02148	23A1		
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	1000	TANK T	nitramb,	T T			
	11111	CANT	AFFLICANI: Blume, John	or hod	4	COMMITTED AND A STATE OF A TRANSPISSORY	, 200 m

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse Gaps .. 0 Length 25; FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25 Indels Sequence 888593, Application US/10719900
Userial No. US20050026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3288.1
CURRENT APPLICATION UNMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20 Score 16.6; DB 13; Pred. No. 8.8e+02; 4; Mismatches 4; 2 GAGAGGGCUGGUUAAGGCGUCC 24 |||||| |:||: ||| |:|| aagaggcccTggTTCAGgAGTCC 69.2**%**; 65.2**%**; Query Match 69.2 Best Local Similarity 65.2 Matches 15; Conservative TYPE: DNA

ORGANISM: Mus musculus
US-11-036-317-713202 RESULT 2 US-10-719-900-888593/c ò g

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APPLICANT: Williams, Alan
APPLICANT: Williams, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
                                                                                                                          Query Match 65.8%; Score 15.8; DB 3; Length 25; Best Local Similarity 73.7%; Pred. No. 2.1e+03; Matches 14; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 751276
LENGTH: 25

    ORGANISM: Artificial Sequence
    FEATURE:
    OTHER INFORMATION: Computer Generated Probe Sequence.
    US-09-940-185-4341

                                                                                                                                                                                                                                                                                                                                                                                                Sequence 751276, Application US/11036317 Publication No. US20050214823A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                2 GAGAGGGCUGGUUAAGGC 20
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5 GAGAGGCGTTGGTTAAGGC 23
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                                                                                                                                                                                                                                                            Length 25;
          PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 888593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Chee, Mark
TITLE OF INVENTION: Probes and Decoder Oligonucleotides;
FILE REPERENCE: A-69605-1;
CURRENT APPLICATION NUMBER: US/09/940,185
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: US 60/227,948
PRIOR APPLICATION NUMBER: US 60/228,854
PRIOR APPLICATION NUMBER: US 60/228,854
PRIOR PILING DATE: 2000-08-25
PRIOR PILING DATE: 2000-08-25
SPIOR PILING DATE: 2000-08-25
SPIOR PILING DATE: 2000-08-25
SPOTWARE: PatentIn version 3.1
SEQ ID NO 365
                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: Computer Generated Probe Sequence. US-09-940-185-365
                                                                                                                                                                                                                                                            DB 9;
                                                                                                                                                                                                                                                            Score 16.2; DB 9;
Pred. No. 1.4e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 365, Application US/09940185
                                                                                                                                                                                                                                                                                                                                                             4 GAGGGCUGGUUAAGGCGUCC 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Publication No. US20030096239A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                            Query Match 67.5%;
Best Local Similarity 66.7%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gunderson, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Conservative
                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-888593
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Matches 14; Conserv
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Length 25;

Score 15.8; DB 13; 2.1e+03;

65.8%;

68.48;

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APPLICANT: Blume, John TITLE OF INVENTIONS. Method of Analysis of Alternative Splicing in Mouse FILE REPERENCE: 3654.1 CURRENT APPLICATION NUMBER: US/11/036,317 CURRENT FILING DATE: 2005-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 25;
                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15.6; DB 13;
Pred. No. 2.6e+03;
                 Sequence 508584, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 63.6
Matches 14, Conservative
                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Mus musculus
US-11-036-317-508584/c
                                                                                                                                                                                                                                                                                                                                                                                 US-11-036-317-508584
                                                                                                                                                                                                                                                                                            SEQ ID NO 508584
LENGTH: 25
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APPLICANT: Chee, Mark
TITLE OF INVENTION: Probes and Decoder Oligonucleotides
FILE REFERENCE: A-69605-1
CURRENT APPLICATION UNMER: US/09/940,185
CURRENT FILING DATE: 2001-08-27

Sequence 4341, Application US/09940185 Publication No. US20030096239A1

GENERAL INFORMATION: APPLICANT: Gunderson, Kevin

PRIOR APPLICATION NUMBER: US 60/227,948
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 60/228,854
PRIOR FILING DATE: 2000-08-29

NUMBER OF SEQ ID NOS: 4768 SOFTWARE: PatentIn version 3.1

SEQ ID NO 4341 LENGTH: 25

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APPLICANT: Benewich, Isaac
APPLICANT: Benewich, Isaac
APPLICANT: Bailer, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and:
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION WUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 310486
LENGTH: 21
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Formarion No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION WINDER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
SOFTWARE: Patentin version 3.3
SEQ ID NO 310487
LENGTH: 21
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Pred. No. 4.1e+03;
                                                                                                                                                                                                     .1e+03
                                                                                                                                                                          Score 15.2; DB Pred. No. 4.1e+2; Mismatches
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 310486, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                        1 UGAGAGGGCUGGUUAAGGC 20
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75.0%;
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75.0%;
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75.0%;
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Best Local Similarity
.....hes 15; Conserv?
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Best Local Similarity
Matches 15; Conserv
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Best Local Similarity
Matches 15; Conserv
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SOFTWARE: Patentin
SEQ ID NO 310485
LENGTH: 21
                                                                                                  , ORGANISM: Human
US-10-310-914A-310485
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                                                                                 TYPE: RNA
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APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
APPLICANT: Bioinformatically detectable group of novel regulatory genes and
ITILE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT PLING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SEQ ID NO 310484
LENGTH: 21
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TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 0600 CPUSO1
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
                                                                                                                                                                        APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
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                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .6e+03;
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Pred. No. 2.
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Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 310484, Application US/10310914A
Publication No. US20060003322A1
                                                                            ; Sequence 648052, Application US/11036317; Publication No. US20050214823A1
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63.6%;
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Best Local Similarity 63.6
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-648052
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Best Local Similarity
Thes 15; Conserve
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APPLICANT: Williams,
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US-10-310-914A-310484/c
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; ORGANISM: Human
US-10-310-914A-310484
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LENGTH: 25
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Search completed: June 19, 2007, 16:27:48 Job time: 1263 secs
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80.0%;
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SOFTWARE: Patentin version 3.3
SEQ ID NO 594065
LENGTH: 24
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Best Local Similarity 80.0
Matches 16; Conservative
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Best Local Similarity
Matches 17; Conserv
                                           , TYPE: RNA
, ORGANISM: Human
US-10-310-914A-1056699
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US-10-310-914A-594065
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SEQ ID NO 1056699
LENGTH: 22
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APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087,0200.CPUS01
CURRENT APPLICATION NUMBER: uS/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
                                                                                                                                                                 APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
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Publication No. US2006000332A1
GENERAL INPOWARTON:
SAPLICANT: Benewich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
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85.0%; Pred. No. 4.1e+03;
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                                                                     Sequence 594029, Application US/10310914A bublication No. US2006003322A1 GENERAL INFORMATION: APPLICANT: Bentwich, Isaac
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Matches 17; Conservative
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US-10-310-914A-1056699/c
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Matches 16; Conserv
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ORGANISM: Human
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 594029
LENGTH: 21
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087-0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
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                                         Gaps
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Length 22;
                                         Indels
, DB 11;
4.1e+03;
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                                                                                                                                                                                                                              Sequence 594065, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
                                                                                   2 GAGAGGGCUGGUUAAGGCG 21
                                                                                                                        21 GAGAAGGCTGGAGAAGGCG
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85.0%;
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Sequence 42828, A Sequence 225295, Sequence 254645, Sequence 40910, A Sequence 2704, Ap

Sequence 187400, Sequence 197873, Sequence 208809, Sequence 494124, Sequence 494904,

Sequence 2706, Ap Sequence 4136, Ap Sequence 11011, A

Sequence:

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Run

Searched:

Database

Sequence 1899145, Sequence 1899145, Sequence 189021, Sequence 189146, Sequence 1856798, Sequence 1969470, Sequence 578997, Sequence 578997, Sequence 578997, Sequence 578997, Sequence 578997, Sequence 1969470, Sequence 1969470, Sequence 1969470, Sequence 578997, Sequence 578997, Sequence 578997, Sequence 578997, Sequence 578997, Sequence 196028, A

Sequence 46048, A Sequence 46028, A Sequence 46048, A

Sequence 1365090,

Sequence 1892935, Sequence 1893092,

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US-10-956-160-156795
US-10-956-160-156795
US-10-956-160-156795
Sequence 156795, Application US/10956160
Publication No. US20070009899A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
TITLE OF INVENTION: WCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
TITLE OF INVENTION: WOBELS OF INFLAWMATORY DISEASES
TITLE REPERRENCE: 031896-044000 (AMN101084)
CURRENT PILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 22274
SOFTWARE: PATENTIN Version 3.2
SEQ ID NO 156795
LENGTH: 25
US-10-709-691B-145999
US-10-709-691B-153005
US-10-709-691B-197400
US-10-709-691B-197400
US-10-709-691B-197401
US-10-709-691B-208809
US-10-709-691B-208809
US-10-709-691B-225295
US-10-859-198-2546910
US-10-859-198-2546910
US-10-859-198-2546910
US-10-859-198-2546910
US-10-859-198-2546910
US-11-509-413-2704
US-11-509-413-2704
US-11-509-413-1366
US-10-709-691B-1899145
US-10-709-691B-1899145
US-10-709-691B-1969470
US-10-709-691B-1969995
US-11-093-832-46048
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Pred. No. 4.9e+03;
; Mismatches 3;
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; Sequence 157603, Application US/10956160
; Publication No. US20070009899A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-156795
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Best Local Simi
Matches 14;
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2: FBMC_Celerra_SIDS3/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
3: FBMC_Celerra_SIDS3/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
4: FBMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
5: FBMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
6: FBMC_Celerra_SIDS3/ptodata/2/pubpna/USO1_NEW_PUB.seq:*
7: FBMC_Celerra_SIDS3/ptodata/2/pubpna/USO1_NEW_PUB.seq:*
8: FBMC_Celerra_SIDS3/ptodata/2/pubpna/USO1_NEW_PUB.seq:*
9: FBMC_Celerra_SIDS3/ptodata/2/pubpna/USO1_NEW_PUB.seq:*
10: FBMC_Celerra_SIDS3/ptodata/2/pubpna/USO1_NEW_PUB.seq6:*
11: FBMC_Celerra_SIDS3/ptodata/2/pubpna/USO1_NEW_PUB.seq6:*
12: FBMC_Celerra_SIDS3/ptodata/2/pubpna/USO1_NEW_PUB.seq6:*
13: FBMC_Celerra_SIDS3/ptodata/2/pubpna/USO1_NEW_PUB.seq6:*
14: FBMC_Celerra_SIDS3/ptodata/2/pubpna/USO1_NEW_PUB.seq6:*
15: FBMC_Celerra_SIDS3/ptodata/2/pubpna/USO1_NEW_PUB.seq6:*
16: FBMC_Celerra_SIDS3/ptodata/2/pubpna/USO1_NEW_PUB.seq6:*
17: FBMC_Celerra_SIDS3/ptodata/2/pubpna/USO1_NEW_PUB.seq6:*
18: FBMC_Celerra_SIDS3/ptodata/2/pubpna/USO1_NEW_PUB.seq6:*
18: FBMC_Celerra_SIDS3/ptodata/2/pubpna/USO1_NEW_PUB.seq6:*
18: FBMC_Celerra_SIDS3/ptodata/2/pubpna/USO1_NEW_PUB.seq6:*
18: FBMC_Celerra_SIDS3/ptodata/2/pubpna/USO1_NEW_PUB.seq6:*
18: FBMC_Celerra_SIDS3/ptodata/2/pubpna/USO1_NEW_PUB.seq6:*
19: FBMC_Celerra_SIDS3/ptodata/2/pubpna/USO1_NEW_PUB.seq6:*
19: FBMC_Celerra_SIDS3/ptodata/2/pubpna/USO1_NEW_PUB.seq6:*
10: FBMC_Celerra_SIDS3/p
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Sequence 1176587,
Sequence 19539, A
Sequence 101448,
Sequence 123481,
Sequence 134127,
Sequence 142127,
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/EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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                                                                                                                                                              June 19, 2007, 13:01:51; Search time 610 Seconds (without alignments) 405.912 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 results predicted by chance to have a
1 to the score of the result being printed,
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                           GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd.
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0 US-110-709-691B-19539

US-10-709-691B-101448

US-10-709-691B-121441

US-10-709-691B-121441

US-10-709-691B-1214127

US-10-709-691B-142124
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US-10-956-160-157603
US-10-956-160-123988
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Listing first 45 summaries
                                                                                                                    OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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24
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Match Length
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Maximum DB seq length: 25
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114.8
114.8
114.2
114.1
114.1
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Gaps

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Length 25; Indels

Result No.

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Gaps
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APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
TITLE OF INVENTION NUMBER: US/10/714,333A
CURRENT APPLICATION NUMBER: 05/502,050
PRIOR FILING DATE: 2003-01-01
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-01-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
APPLICANT: Scaringe, Stephen
TILLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REPERENCE: 13499US
   Score 14.4; DB 9;
Pred. No. 1.1e+04;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .4e+04;
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PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR PILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
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CURRENT FILING DATE: 2005-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1176587, Application US/10714333A Publication No. US20070031844A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1176587, Application US/11093832 Publication No. US20070039072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 cacaccuccuccunaaacc 19
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Reynolds, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.2%;
Query Match 60.0%;
Best Local Similarity 75.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1176587
LENGTH: 19
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US-10-714-333A-1176587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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Publication No. US20070031843A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL OF INVENTION:
APPLICANT:
APPLICAN
                                       DETECTING GENE EXPRESSION IN ANIMAL DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 15.2; DB 11; Length 25; Pred. No. 4.9e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 123988, Application US/10956160
Publication No. US20070009899A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Woute, William M
APPLICANT: Mounts, William M
TITLE OF INVENTION: MOCLEIC ACID ARRAYS FOR DET
TITLE OF INVENTION: MODELS OF INFLAMMATORY DIS
FILE REFERENCE: 031896-044000 (AMI01084)
CURRENT APPLICANTION NUMBER: US/10/956,160
CURRENT PILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 222274
SOFTWARE: Patentin version 3.2
SEQ ID NO 123988
LENGTH: 25
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                   APPLICANT: Mounts, William M
IITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR
IITLE OF INVENTION: MODELS OF INFLAMMATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/709,691B
CURRENT FILING DATE: 2004-05-24
NUMBER OF SEQ ID NOS: 4254815
                                                                                                                      FILE REFERENCE: 031896-044000 (AMILLOB4)
CURRENT APPLICATION NUMBER: US/10/956,160
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 222274
SOFTWARE: PatentIn version 3.2
LENGTH: 25
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; ORGANISM: Neisseria meningitidis Z2491
US-10-709-691B-1378586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 GAGGGCUGGUUAAGGCGUC 23
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SEO ID NO 1378586
LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA; Canis familiaris
US-10-956-160-157603
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Sequence 123481, Application US/10709691B
Publication No. US20070031843A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Itzhak
APPLICANT: Bentwich, Itzhak
APPLICANT: Anniel, Amir
TITLE OF INVENTION: Bioinformatically Detectable Group of Novel Regulatory Bacterial
TITLE OF INVENTION: and Bacterial Associated Oligonucleotides and Uses Thereof
FILE REPERENCE: Efe23
CURRENT PAPLICATION NUMBER: US/10/709,691B
CURRENT FILING DATE: 2004-05-24
NUMBER OF SEQ ID NOS: 4254815
SEQ ID NO 123481
LENGTH: 22
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US-10-709-691B-134127/c
Sequence 134127, Application US/10709691B
Publication No. US20070031843A1
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
APPLICANT: ROSETTA Amin
TITLE OF INVENTION: Bloinformatically Detectable Group of Novel Regulatory Bacterial
TITLE OF INVENTION: and Bacterial Associated Oligonucleotides and Uses Thereof
FILE REFERENCE: Efs23
CURRENT APPLICATION WUBBER: US/10/709,691B
CURRENT FILING DATE: 2004-05-24
NUMBER OF SEQ ID NOS: 4254815
SOFTWARE: PatentIn version 3.3
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APPLICANT: ROSETTA GENOMICS LTD
APPLICANT: Bentwich, Itzhak
APPLICANT: Bentwich, Itzhak
APPLICANT: Bentwich, Itzhak
APPLICANT: Bentwich, Itzhak
APPLICANT: Avniel, Amir
TITLE OF INVENTION: Bioinformatically Detectable Group of Novel Regulatory Bacterial
TITLE OF INVENTION: and Bacterial Associated Oligonucleotides and Uses Thereof
FILE REFERENCE: Efea3
CURRENT APPLICATION NUMBER: US/10/709, 691B
CURRENT APPLICATION NUMBER: US/204-05-24
NUMBER OF SEQ 1D NOS: 4254815
SOFTWARE: Patentin version 3.3
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Pred. No. 1.8e+04;
3; Mismatches 0;
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Pred. No. 1.8e+04;
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; Sequence 142124, Application US/10709691B
; Publication No. US20070031843A1
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78.6%;
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Best Local Similarity 78.6
Matches 11; Conservative
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Best Local Similarity
Matches 11; Conserv
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US-10-709-691B-123481
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US-10-709-691B-134127
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                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: RNA
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Fublication No. US20070031843A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
APPLICANT: Bentwich, Itzhak
APPLICANT: Avniel, Amir
TITLE OF INVENTION: Bioinformatically Detectable Group of Novel Regulatory Bacté;
TITLE OF INVENTION: Bioinformatically Associated Oligonucleotides and Uses Thereof;
TITLE OF INVENTION: 2014-05-24
NUMBER OF SEQ ID NOS: 4254815
SEQ ID NO: 4254815
SEQ ID NO: 9539
LENGTH: 22
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; Publication No. US20070031843A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
APPLICANT: Bentwich, Itzhak
TITLE OF INVENTION: Bioinformatically Detectable Group of Novel Reg
TITLE OF INVENTION: Bioinformatically Associated Oligonucleotides and
FILE REFERENCE: Efs23
CURRENT APPLICATION NUMBER: US/10/709,691B
CURRENT FILLING DATE: 2004-05-24
NUMBER OF SEQ ID NOS: 4254815
SOFTWARE: PatentIn version 3.3
SEQ ID NO 101448
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                                                         Score 14.2; DB 17; Length 19; Pred. No. 1.4e+04; 0; Mismatches 3; Indels C
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78.6%; Pred. No. 1.8e+04;
tive 3; Mismatches 0
                                                                                                                                                                     2 GAGAGGGCUGGUUAAGGC 20
                                                                                                                                                                                                                       1 GAGAGCAGCUGGUUAAAGC 19
                                                                 Query Match 59.2%;
Best Local Similarity 84.2%;
Matches 16; Conservative
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Best Local Similarity 78.6%;
Matches 11; Conservative
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Best Local Similarity 78.6
Matches 11; Conservative
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US-10-709-691B-123481/c
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; ORGANISM: Human
US-10-709-691B-101448
               US-11-093-832-1176587
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; ORGANISM: Human
US-10-709-691B-19539
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Sequence 197833, Application US/10709691B
; Sequence 197833, Application US/10709691B
; Publication No. US20070031843A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Bentwich, Itzhak
; TITLE OF INVENTION: Bioinformatically Detectable Group of Novel Regulatory Bacturi TITLE OF INVENTION: and Bacterial Associated Oligonucleotides and Uses Thereof; TITLE OF INVENTION UNMER: US/10/709,691B
; CURRENT APPLICATION NUMBER: US/10/709,691B
; CURRENT PILING DATE: 2004-05-24
; NUMBER OF SRQ ID NOS: 4254815
; SEQ ID NO 197873
; LENGTH: 22
; LENGTH: 22
                                                                                                                                                                                Sequence 187400, Application US/10709691B

| Bublication No. US2070031843A1 |
| Charleston No. US2070031843A1 |
| APPLICANT: Robert No. US20710 |
| TITLE OF INVENTION: Bioinformatically Detectable Group of Novel Regulatory Bacter ITLES OF INVENTION: and Bacterial Associated Oligonucleotides and Uses Thereof |
| TITLE OF INVENTION: Bioinformatically Detectable Group of Novel Regulatory Bacter ITLES OF INVENTION UNMER: 0204-05-24 |
| CURRENT PAPLICATION NUMBER: 0204-05-24 |
| NUMBER OF SEQ ID NOS: 4254815 |
| SEQ ID NO 187400 |
| LENGTH: 22 |
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Job time : 612.5 secs
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Best Local Similarity 78...
Local 11; Conservative
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Matches 11; Conservative
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; ORGANISM: Human
US-10-709-691B-187400
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ORGANISM: Human
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Publication No. US20070031843A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
APPLICANT: Bentwich, Itchak
APPLICANT: Arniel, Amir
APPLICANT: Arniel, Amir
APPLICANT: Anniel, Amir
APPLICANT: Arniel, Ami
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CURRENT FILING DATE: 2004-05-24
NUMBER OF SEQ ID NOS: 4254815
SOFTWARE: Patentin version 3.3
SEQ ID NO 145999
LENGTH: 22
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Best Local Similarity 78.6°
Matches 11, Conservative
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Best Local Similarity 78.6
Matches 11; Conservative
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US-10-709-691B-153005/c
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US-10-709-691B-153005
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                                                                                                               TYPE: RNA
ORGANISM: Human
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ORGANISM: Human
; SEQ ID NO 142124
; LENGTH: 22
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10.4 43.3 19 15 AZ595016 AZ59501 10.4 43.3 22 1 AA978171 AA978171 10.4 43.3 24 15 AZ786207 AZ33132 10.2 42.5 19 15 AZ331326 AZ334544 10.2 42.5 19 15 AZ34549 AZ34541 10.2 42.5 19 15 AZ345531 AZ34551 10.2 42.5 19 15 AZ345536 AZ34557 10.2 42.5 19 15 AZ345570 AZ345571 10.2 42.5 19 15 AZ345709 AZ346701	10.2 42.5 19 15 AZ36887 10.2 42.5 19 15 AZ36887 10.2 42.5 19 15 AZ447247 10.2 42.5 19 15 AZ510096 10.2 42.5 19 15 AZ510106 10.2 42.5 19 15 AZ510106 10.2 42.5 21 15 AZ510134 10.2 42.5 21 15 AZ510134 10.2 42.5 21 15 AZ64549	10.2 42.5 21 15 AZ850337 AZ85033 AZ85033 10.2 42.5 22 15 AZ85031 AZ85033 AZ85033 10.2 42.5 22 15 AZ85033 AZ85033 AZ85033 10 41.7 20 15 AZ817235 AZ31842 AZ89628 AZ8962	10 41.7 25 15 AZ611099 AZ611099 IM0436K1 10 41.7 25 15 AZ772979 AZ772979 IM0584E1 ALIGNMENTS	AZ8 C10 AZ8 AZ8 GSS Mus Mus Buk Mam		University of Utah University of Utah Rm. 308, Biomedical 84112, USA Tel: 801 585 5606 Fax: 801 585 5606 Fax: 801 585 7177 Email: ddunn@geneti Insert Length: 1000 Plate: 0068 row: F Seq primer: CGTTGTA Class: plasmid ends High quality sequen Location/Q
	000000000	Ω Ω ω ω ω ω ω ω 4 4 4 4 4 π φ Γ φ φ φ Ο Η α κ	4 4 5	RESULT 1 AZB06300 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES
on 6.2.1 Biocceleration Ltd. Search time 6876 Seconds (Without alignments)		eters: 35954			dicted by chance to have a re of the result being printed, I score distribution.	AZ80500 ZM0068F13 AZ80501 ZM0068F13 AZ89603 YP91b12.T. R89803 YP91b12.T. AZ654730 1M0529P05 AZ794596 ZM0092001 AZ820085 ZM0092001 AZ843166 1M037R05 AZ83166 1M037R05 AZ836049 ZM0146810 AZ84516 1M0327R05 AZ8451729 1M008Z810 AZ846729 1M008Z810 AZ851549 ZM0153P13
GenCore version Copyright (c) 1993 - 2007 OM nucleic - nucleic search, using sw model Run on: June 19, 2007, 12:49:12; Sea	Title: US-10-604-726A-6034 Perfect score: 24 Sequence: 1 ugagagggggggggggggggggggggggggggggggg	Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 25 Post-processing: Minimum Match 0% Maximum Maximum Match 100% Listing first 45 summaries		6: 9D htc:* 7: 9D_est2:* 8: 9D_est2:* 9: 9D_est7:* 10: 9D_est13:* 11: 9D_est13:* 13: 9D_est12:* 14: 9D_est10:* 16: 9D_9ss1:* 17: 9D_9ss3:* 19: 9D_9ss3:* 19: 9D_9ss5:*	Pred. No. is the number of results predicted by score greater than or equal to the score of the and is derived by analysis of the total score d summaries * Result Query No. Score Match Length DB ID	12.6 12.6 12.5 10.6 11.6 48.3 11.2 46.7 11.2 46.7 11.2 46.7 11.2 11.4

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DEFINITION
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JOURNAL
COMMENT
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R89803/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                            (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.5 Kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD4 (gi|4732114 |gb|AF129072.11), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptorebent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing Dy: Washington University Genome Sequencing Center
Clone distribution: NCI-CARP Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 09-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Buarchontoglires, Primates, Haplorrhini, Catarrhini, Hominidae, Homo.

(Patarrhini, Hominidae, Homo.

(Pases 1 to 22)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AI473941 22 bp mRNA linear EST 09-MAR-19
tm04c11.x1 NCI CGAP Co14 Homo sapiens cDNA clone IMAGE:2155604 3'
similar to TR:Q06459 Q06459 NUCLEOLIN. ;, mRNA sequence.
                                                                                                                                                                                 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                  lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
                                                                                                                                                              'clone_lib="Mouse 10kb plasmid UUGCIM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.5%; Score 12.6; DB 15; Length 24; 57.9%; Pred. No. 7.7e+05; ive 4; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ww-bio.llnl.gov/bbrp/image/image.html
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Seg primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualiflers
type="genomic DNA"
ain="C57BL/6J"
                                                    db_xref="taxon:10090"
                                                                             clone="UUGC2M0068F13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .22
/organism="Homo s
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 UGAGAGGGCUGGUUAAGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :| ||| || :|| ||
5 TGGGAGTGGGTGGTTAGGG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI473941.1 GI:4326986
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
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AUTHORS
TITLE
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="20 week-post conception fetus"

/lab host="DH10B (ampicillin'realstant)"
/clone lib="Sozues fetal liver spleen lNFLS"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site l: Pac I; Site 2: Eco RI;
lst strand cDNA was primed with a Pac I - oligo(dT) primer
[5: ACTGGBAGAATTAAAGATCTTTTTTTTTTTTTTTTT] 3:],
                                                                         /clone_lib="NCI_CGAP_CO14"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Sal1;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.7 kb. Life Technologies catalog #:
11531-019"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

(bases 1 to 25)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hulman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                    /clone="IMAGE:2155604"
/tissue_type="moderately-differentiated adenocarcinoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1193 Std Error: 0.00
Seq primar: MI3RP1
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wastson.wustl.edu
Insert Size: 1193
                                                                                                                                                                                                                                                                                                        Score 12; DB 1; Length 22; Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="GDB:3763833"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db_xref="taxon:9606"
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xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                              2 GAGAGGGCUGGUUAAGGCG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 GAGAGGGGAGGTCGAGGGG 1
                                                                                                                                                                                                                                                                                                        50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R89803.1 GI:954630
                                                                                                                                                                                                                                                                                                                                                                   14; Conservative
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Best Local Similarity
Matches 14; Conserv
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ORIGIN

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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ654730 21 bp DNA linear GSS 14-DEC-2000 1M0529P05F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0529P05 F, genomic survey sequence.
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electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polynuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euarchontoglires; Glires; Rodentia;
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodent
                                                                                                                                                                                             Score 12; DB 11; Length 25;
Pred. No. 1.4e+06;
3; Mismatches 0; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0529 row: P column: 05
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="UUGC1M0529P05"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
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                                                                                                                                                                                             50.0%;
75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rm. 308, Biomedical
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
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12 GGGCTGGTTAA 1
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Best Local Similarity
Matches 9; Conserv
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DEFINITION
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inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ794596 25 bp DNA linear GSS 16-FEB-200
2M0048M20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 25)
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/clone llb="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone UUGC2M0048M20 F, genomic survey sequence
                                                                                                                                                                                                DB 15;
                                                                                                                                                                                                Score 11.6; DB 15,
Pred. No. 2.1e+06;
2; Mismatches 4,
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Insert Length: 10000 Std Error: 0.00
Plate: 0048 row: M column: 20
Seg primer: CGTYCTAAAACGACGGCCAGT
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/strain="C57BL/6J"
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/clone="UUGC2M0048M20"
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Location/Qualifiers
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                                                                                                                                                                                                                                                Conservative
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Fax: 801 585 7177
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Best Local Similarity
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ORIGIN

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of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X1.10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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                                                                                                                                                                                                                         47.5%; Score 11.4; DB 15; Length 25; larity 57.1%; Pred. No. 2.6e+06; Conservative 3; Mismatches 6; Indels
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mol_type="genomic DNA"
strain="C57BL/6J"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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clone="UUGC1M0073B16"
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Insert Length: 10000 Std Erro:
Plate: 0073 row: B column: 16
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High quality sequence stop: 24.
Location/Qualifiers
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Fax: 801 585 7177
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Mus musculus
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0092001F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0092001 F, genomic survey sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroldea; Muridae; Murinae; Mus.
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Pred. No. 3.2e+06;
2; Mismatches 3;
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Fax: 801 585 7177
Email: ddunnagenetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0092 row: O column: 01
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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Seg primer: CGTTGTAAAACGACGGCCAGT
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University of Utah Genome Center
University of Utah
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/clone="UUGC2M0092001"
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Location/Qualifiers
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Best Local Similarity 68.8%;
Matches 11; Conservative 2
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KEYWORDS
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10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gl[4732114] [gp]AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XII.0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
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Insert Length: 10000 Std Error: 0.00
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Seq primer: CACACAGGAAACAGCTATGACC

    .20
    /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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High quality sequence stop: 20.
Location/Qualifiers
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/clone="UUGC2M0146E10"
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Fax: 801 585 7177
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Best Local Similarity
Matches 11; Conserva
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adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi]4732114 [pb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XII.0-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0327K05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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84112, USA
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/note="Voctor: PWD4ZIX; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Kose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0327 row: K column: 05
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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    .21
    /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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clone="UUGC1M0327K05"
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4
ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalouible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored ovector NA, and transformed into chemically-competent E. coli Xiio-Gold (Stratagene) cells and selected for ampicillin resistance."
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clab host="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jacksor Laboratory Mouse DNA Resource
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1 (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
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45.8%; Score 11; DB 15; Length 21;
Best Local Similarity 57.9%; Pred. No. 3.9e+06;
Matches 11; Conservative 3; Mismatches 5; Indels
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0130 row: E column: 11
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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|strain="C57BL/6J"
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'c1one="UUGC2M0130E11"
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SOURCE
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polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 |gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resources
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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84112, USA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Fax: 801 585 7177
Email: ddunm@genetics.utah.edu
Email: ddunm@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0206 row: L column: 22
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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Contact: Robert B. Weiss
University of Utah Genome Center
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AUTHORS
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was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high modar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi |472114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

1 (bases 1 to 22)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
This clone is available royalty-free through LLNL, contact the
IMAGE Consortium (inft@eimage.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 698 Std Brror: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                  Score 11; DB 15; Length 25;
Pred. No. 4e+06;
3; Mismatches 5; Indels
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/db_xref="taxon:9606"
/clone="IMAGE:1732030"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI183338.1 GI:3733976
                                                                                                                                                                                                                                                                                                                                           ch 45.8%;
1 Similarity 57.9%;
11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 11; Conserva
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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purifier agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells
                                                                                                                                                                                                                                                                                                       AZ346729 20-SEP-2000 1M0082A10F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0082A10 F, genomic survey sequence.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM ibrary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb
                                                           Gaps
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     Length 22;
     DB 1;
Score 10.8; DB 1;
Pred. No. 4.9e+06;
3; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0
Plate: 0082 row: A column: 10
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db xref="taxon:10090"
/clone="UUGC1M0082A10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                     AZ346729.1 GI:10425966
        45.0%;
                                                                                                                2 GAGAGGGCUGGUU 15
                                                                                                                                                                   17 GAGTGGGGTGGTT 4
                                                             9; Conservative
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Unpublished (2000)
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Fax: 801 585 7177
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  Query Match
Best Local Similarity
Matches 9; Conserv
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AZ346729/c
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SOURCE
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Query Match
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Matches 11, Conserv
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AZ595016/c
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AUTHORS
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2M0153P13R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0153P13 R, genomic survey sequence.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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/clone lib="Mouse 10kb plasmid UNGCIM library"
/note="Vector: PWD42Iv; Purified genomic DNA from M.
musculus C57BL/6J (malle) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 25)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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                                                                      Length 20;
                                                                                                                        Indels
and selected for ampicillin resistance."
                                                                      44.2%; Score 10.6; DB 15;
64.7%; Pred. No. 5.9e+06;
tive 2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0153 row: P column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory Mouse DNA Resource
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University of Utah Genome Center
University of Utah
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strain="C57BL/6J"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ851549.1 GI:13037657
                                                                                                                                                                        2 GAGAGGGCUGGUUAAG 18
                                                                                                                                                                                                                     20 GAGTGAGGTTGGTGAAG 4
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                                                                                                                        11; Conservative
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Fax: 801 585 7177
                                                                                                    Best Local Similarity
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                                                                        Query Match
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AZ851549/c
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ORGANISM
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KEYWORDS
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 (gil 4732114 |gb| AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Musinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi,A., Barber,M., Baccorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ595016 119 bp DNA linear GSS 13-DEC-200 1M0407C19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0407C19 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                                                                                                                                        Gaps
                                                                                                                                                                                        ö
                                                                                                                         Length 25
                                                                                                                                                                                        Indels
                                                                                                             Score 10.6; DB 15;
Pred. No. 6e+06;
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Fax: 801 585 7177

Email: ddun@qenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0407 row: C column: 19
Seq primer: CGTTGTAAAACGACGGCCAGT
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0407C19"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                     2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ595016.1 GI:11717206
GSS.
                                                                                                                                                                                                                                                3 AGAGGGCCUGGUUAAGG 19
                                                                                                                            44.2%;
64.7%;
                                                                                                                                                                                                                                                                                  25 AGAAGGTAAGGTTAAGG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class: plasmid ends
                                                                                                                                                                                        11; Conservative
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adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

0; Gaps Query Match
43.3%; Score 10.4; DB 15; Length 19;
Best Local Similarity 75.0%; Pred. No. 7.3e+06;
Matches 9; Conservative 2; Mismatches 1; Indels (

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1 UGAGAGGGGCUG 12

:| ||||||:| 17 TGGAGGGGCTG 6

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Search completed: June 19, 2007, 20:24:43 Job time : 6878 secs